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UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 C.F.R. 1.53(b))

Attorney Docket No.	2631.1002-001
First Named Inventor or Application Identifier	Raymond J. Dattwyler
Express Mail Label No.	EL387775380US

Title of Invention

Groups of Borrelia Burgdorferi And Borrelia Afzelii That Cause Lyme Disease In Humans

APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents.

ADDRESS TO:

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1. ☐ Fee Transmittal Form
(Submit an original, and a duplicate for fee processing)
2. ☒ Specification [Total Pages [55]]
(preferred arrangement set forth below)
 - Descriptive title of the invention
 - Cross References to Related Applications
 - Statement Regarding Fed sponsored R & D
 - Reference to microfiche Appendix
 - Background of the Invention
 - Summary of the Invention
 - Brief Description of the Drawings
 - Detailed Description
 - Claim(s)
 - Abstract of the Disclosure
3. ☒ Drawing(s) (35 U.S.C. 113) [Total Sheets [8]]
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4. ☐ Oath or Declaration/POA [Total Pages []]
a. ☐ Newly executed (original or copy)
b. ☐ Copy from a prior application (37 C.F.R. 1.63(d))
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[NOTE Box 5 below]
i. ☐ DELETION OF INVENTOR(S)
Signed statement attached deleting inventor(s) named in the prior application, see 37 C.F.R. 1.63(d)(2) and 1.33(b).
5. ☐ Incorporation By Reference (useable if Box 4b is checked)
The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under Box 4b, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.

6. ☐ Microfiche Computer Program (Appendix)
7. ☒ Nucleotide and/or Amino Acid Sequence Submission
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ACCOMPANYING APPLICATION PARTS

8. ☐ Assignment Papers (cover sheet & documents)
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Prior application information: Examiner:

Group Art Unit:

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Attorney's Docket No.: 2631.1002-001

GROUPS OF *BORRELIA BURGDORFERI* AND *BORRELIA AFZELII*
THAT CAUSE LYME DISEASE IN HUMANS

RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application No.

- 5 60/140,042, filed June 18, 1999, the entire teachings of which are incorporated herein
by reference in their entirety.

GOVERNMENT SUPPORT

- The invention was supported, in whole or in part, by grant AIAR37256 from
The National Institutes of Health, grant RO1AI33454 from the National Institute of
10 Infectious Disease and cooperative agreement number U50/CCU210518 from the
Centers for Disease Control. The Government has certain rights in the invention.

BACKGROUND OF THE INVENTION

- Lyme disease begins at the site of a tick bite, producing a primary infection with
spread of the organism to secondary sites occurring early in the course of infection.
15 Lyme disease is a progressive multi-system disorder and is the most common vector-
borne disease in both North America and Europe. This disease was first described as a
focus of pediatric arthritis patients in Old Lyme, CT (Steere, A.C., *et al.*, *Arth. Rheum.*

20:17 (1977)). The association of this syndrome with the bite of the deer tick, *Ixodes scapularis*, led to the identification of the spirochete *Borrelia burgdorferi* as the causative agent (Burgdorfer, W., *et al.*, *Science*, 216:1317-1319 (1982)). As culture isolation of the bacterium from clinical and field samples became more efficient,

- Baranton and colleagues described three pathogenic genospecies, *B. Burgdorferi* sensu stricto (*B. Burgdorferi* or *B.b.s.s.*), *B. afzelii*, and *B. garinii* (Baranton, G., *et al.*, *Int. J. Syst. Bacteriol.* 42:378-383 (1992)). These are members of a species complex, *B. burgdorferi* sensu lato, which consists of at least 10 different genospecies (Piken, R.N., *et al.*, *J. Invest. Dermatol.*, 110:211-214 (1998); Postic, D., *et al.*, *Int. J. Syst. Bacteriol.* 44:743-752 (1994); Valsangiacomo, C.T., *et al.*, *Int. J. Syst. Bacteriol.* 47:1-10 (1997)). *B. Burgdorferi*, *B. afzelii* and *B. garinii* are thought to be pathogenic and all are found in Europe, but in North America, *B. burgdorferi* is the only pathogenic genospecies found. Each of these three genospecies is associated with distinct clinical manifestations (Van Dam, A. P. *et al.*, *Clin. Infect. Dis.* 17:708-717 (1993)). This implies that differences in genospecies may play an important role in the wide array of clinical manifestations observed in Lyme Disease.

As an infected tick begins to feed on a mammal, the synthesis of outer surface protein C (OspC) is induced (Schwan, T.G., *et al.*, *Proc. Natl. Acad. Sci.* 2:2909-2913 (1995)). Thus, in early infection, OspC is the major outer membrane protein expressed by the spirochete (Fung, B.P., *et al.*, *Infect. Immun.* 62:3213-3221 (1994); Padula, S.J., *et al.*, *J. Clin. Microbiol.*, 32:1733-1738 (1994)). Even though OspC has been demonstrated to have limited surface exposure (Cox, D.L., *et al.*, *Proc. Natl. Acad. Sci.*, 93:7973-7978 (1996); Mathiesen, M. M., *et al.*, *Infect Immun.* 66:4073-4079 (1998)), OspC is a potent immunogen. Immunization with OspC is protective against tick-transmitted *Borrelia* infection (Gilmore Jr., R.D., *Infect Immun.* 64:2234-2239 (1999)). However, because OspC is highly variable in its sequence, the protection is limited to the *Borrelia burgdorferi* strain expressing the same immunizing OspC encoded by a specific allele. Challenge with heterologous isolates, expressing other *ospC* alleles

results in infection (Probert, W.S., *et al.*, *J. Infect. D.*, 175:400-405 (1997)). OspC is very diverse (Jauris-Heipke, S., *et al.*, *Med. Microbiol. Immunol.* 182:37-50 (1993)). Livey *et al.* found thirty-four alleles in seventy-six *B. burgdorferi sensu lato* isolates (Livey, I., *et al.*, *Mol. Microbiol.* 18:257-269 (1995)).

5 Currently, Lyme Disease is treated with antibiotics. However, such treatment is not always successful in clearing the infection. Treatment is often delayed due to improper diagnosis with the deleterious effect that the infection proceeds to a chronic condition, where treatment with antibiotics is often not useful. One of the factors contributing to delayed treatment is the lack of effective diagnostic tools. W

10 Furthermore, while antigens such as OspC are known to be protective, in some cases the existence of multiple alleles of these antigens greatly hinders the development of vaccines based on such antigens that would protect against more than one strain of *Borrelia*. Two independent trials of first generation vaccines for the prevention of Lyme disease, recently studied the efficacy and safety of a vaccine that is based on
15 recombinant outer surface protein A (OspA) (Sigal, L.H. *et al.*, *N. Engl. J. Med* 339:216-222, 1998; Steere, A.C. *et al.*, *N. Engl. J. Med.* 339:209-215, (1998)). However, a vaccine that consists of recombinant OspA may require frequent booster immunizations. Natural infection with *B. burgdorferi* does not elicit an antibody response to OspA, as it does against OspC. What is needed is a selection of *Borrelia*
20 antigens that can be used to either diagnose or vaccinate against all or most forms of *Borrelia* that cause systemic disease.

Differences in the frequency of *B. burgdorferi*, *B. garinii*, and *B. afzelii* in ticks and human infection has lead to the hypothesis that the different genospecies are differentially pathogenic (Picken, R.N. *et al.*, *J. Invest. Dermatol.* 110:211-214, 1998; 25 Van Dam, A.P. *et al.*, *Clin. Infect. Dis.* 17:708-717, 1993). Nevertheless, the number of different strains within a given genospecies and the differences between the strains of a given genospecies as well as between genospecies impose obstacles in the development of immunogenic protein compounds for use as diagnostic and vaccine agents in the

detection, prevention and treatment of Lyme disease. A number of investigators have used OspC as a serodiagnostic antigen for early Lyme disease (Fung, B.P. *et al.*, *Infect. Immun.* 62:3213-3221, 1994; Gerber, M.A. *et al.*, *J. Infect. Dis.* 171:724-727, 1995; Padula, S.J. *et al.*, *J. Clin. Microbiol.* 32:1733-1738, (1994)). In these tests, the use of

5 OspC as a diagnostic antigen gave highly specific, but not sensitive results. However, these studies included only one *B. burgdorferi* strain and therefore only one type of OspC. Routine tests for the diagnosis of Lyme disease also use a single strain protocol and therefore a single OspC allele for detection of antibody to the spirochete. It is not clear what mixture of OspC proteins must be used to make useful diagnostic and

10 vaccine tools, effective against more than one Lyme disease causing strains of *Borrelia*, if not against most if not all of the invasive strains within a genospecies. Preferably, such a mixture would be effective against all invasive strains of Lyme disease *causing borrelia*.

SUMMARY OF THE INVENTION

15 The present invention is drawn to a composition comprising OspC polypeptides from Lyme Disease causing *Borrelia*. In one embodiment, the composition of the present invention comprises an OspC polypeptide or fragment thereof from at least two *Borrelia burgdorferi* OspC families selected from the group consisting of A, B, I and K, excepting the combination consisting of two OspC proteins, wherein one OspC protein

20 is from OspC family A and the second OspC protein is from OspC family I. In another embodiment, the composition of the present invention comprises at least one OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families A and B.

The present invention is also drawn to a method of immunizing an animal against Lyme disease, comprising administering a composition comprising OspC

25 polypeptides from Lyme Disease causing *Borrelia*. In one embodiment of the present invention, the composition comprises a OspC polypeptide or fragment thereof from at least two *Borrelia burgdorferi* OspC families selected from the group consisting of: A,

B, I and K, excepting the combination consisting of two OspC proteins, wherein one OspC protein is from OspC family A and the second OspC protein is from OspC family I. In another embodiment of the present invention, the composition comprises at least one OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families A and B. The composition of the present invention together with suitable excipients and/or adjuvants is administered to an animal such that the animal develops an immune response to at least one OspC polypeptide of the composition.

The present invention is also drawn to a method of detecting an immune response to Lyme Disease causing *Borrelia* in a host sample. The method comprises contacting a host sample with a composition comprising OspC polypeptides from Lyme disease causing strains of *Borrelia*, such that anti-OspC antibodies, if present, in said sample bind to said OspC polypeptides. In one embodiment, the composition comprises at least one OspC polypeptide or fragment thereof from each of *Borrelia burgdorferi* OspC families A, B, I and K. The amount of antibodies that have bound said OspC polypeptides or fragments thereof are measured; thereby detecting an immune response to Lyme disease causing *Borrelia*.

The present invention is also drawn to a diagnostic kit comprising OspC polypeptides from Lyme Disease causing *Borrelia*. In one embodiment of the present invention, the diagnostic kit comprises at least one OspC polypeptide or diagnostic fragment thereof from each of *Borrelia burgdorferi* OspC families A, B, I and K. In another embodiment of the present invention, the diagnostic composition comprises at least one OspC polypeptide or diagnostic fragment thereof from each of *Borrelia afzelii* OspC families A and B.

In other embodiments of the present invention, the composition comprises at least one OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families A and B. In still other embodiments, the composition comprises OspC polypeptides or fragments thereof from *Borrelia burgdorferi*, *Borrelia afzelii*, *Borrelia garinii* and combinations thereof.

The present invention is also drawn to chimeric proteins for use in the methods of the present invention. In one embodiment, the present invention is drawn to a chimeric protein comprising OspC polypeptides from two or more OspC families of Lyme Disease causing *Borrelia*. In one embodiment, the families comprise *Borrelia burgdorferi* OspC families A, B, I and K. In other embodiment, the families comprise *Borrelia afzelii* OspC families A and B. In still other embodiments, the composition comprises chimeric OspC polypeptides or fragments thereof from *Borrelia burgdorferi*, *Borrelia afzelii*, *Borrelia garinii* and combinations thereof.

The chimeric proteins of the present invention comprise at least a first and a second polypeptide of OspC, such that the first polypeptide comprises OspC from about base 26 to about base 630 of a first *ospC* gene and the second polypeptide comprises about base 28 to about base 570 of a second *ospC* gene. The chimeric proteins of the present invention can be used in the immunization and detection methods of the present invention.

The present invention provides the minimum number of *Borrelia burgdorferi* and *Borrelia afzelii* families that are responsible for systemic disease in humans and is useful for vaccines and diagnostic kits. The present invention provides a combination of proteins that, when used as a vaccine, prevent Lyme disease from becoming systemic. The proteins and chimeric proteins of the present invention can be effective in preventing of Lyme disease as well as having a therapeutic effect on established infection, for example after the tick bite is noticed by the patient. The proteins and chimeric proteins of the present invention are expected to act at the level of the tick as well as the level of the host in preventing both infection and disease due to *Borrelia burgdorferi*, *Borrelia afzelii* and/or *Borrelia garinii*. The present invention allows the development of a worldwide vaccine comprising only six proteins necessary to generate a protective immune response against all pathogenic strains of *Borrelia burgdorferi* and *Borrelia afzelii*.

The present invention also provides improved diagnostic tools. Because of the present invention, it is now possible to prepare diagnostic tools comprising OspC antigens representing the four pathogenic families of *Borrelia burgdorferi* and/or the two pathogenic families of *Borrelia afzelii*, thereby detecting clinically important exposure to pathogenic bacteria while overlooking the remainder of the families which do not cause pathogenic disease.

As demonstrated herein, a significant proportion, if not all, systemic *B. burgdorferi* sensu stricto infections in humans are associated with four *ospC* groups and that a significant portion, if not all, systematic *B. afzelii* infections in humans are associated with two *ospC* groups. Vaccines against OspC are known to be protective, but have been limited by the diversity of *ospC* (Probert, W.S. *et al.*, *J. Infect. D.* 175:400-405, (1997)). The polypeptides of the present invention provide immunogenic proteins, fragments and chimeric proteins thereof for highly protective vaccines and diagnostics. The present invention provides a vaccine that includes one or more of these four forms of OspC. The vaccines of the present invention should be an important second level of protection against disseminated infection of the *B. burgdorferi* spirochete. Furthermore, single-stranded conformational polymorphism (SSCP) analysis described herein may provide a rapid and powerful tool to monitor vaccine efficacy by detecting rare or new invasive *ospC* groups.

New diagnostic assays of the present invention, based on major *ospC* groups A, B, I, and K are useful to identify those at risk for progressive illness. Given that OspC proteins are antigenically variable, individuals infected with one strain may produce an antibody response that is not reactive with an OspC protein from a different major group. Antibody detection using antigen preparations of the present invention, incorporating a proper mix of invasive clones of *B. burgdorferi* will be much more sensitive than the present, single strain protocols. The compositions of the present invention not only elicit humoral and cell mediated immune responses, the

compositions of the present invention are also capable of detecting both humoral and cell mediated immune response when used to test a host sample.

The present invention provides both lipidated OspC polypeptides, fragments thereof and chimeric proteins comprising two or more OspC polypeptides, wherein the chimeric protein has a lipidation signal, such as the lipidation signal from outer surface protein B at the 5' terminus of the gene encoding the chimera. Furthermore, the present invention provides unlipidated OspC polypeptides, fragments thereof and chimeric proteins comprising two or more OspC polypeptides, wherein the gene encoding the chimeric protein does not comprise a lipidation signal and the chimeric protein is not lipidated. Unlipidated OspC polypeptides, fragments thereof and chimeric proteins thereof are advantageous due to simpler production methods, improved yields of protein and simpler purification. The unlipidated chimeric proteins of the present invention unexpectedly elicit an immune response against Lyme disease causing strains of *Borrelia* at least as broadly reactive as lipidated OspC proteins that are used as a positive control. Furthermore, the unlipidated OspC chimeric proteins of the present invention elicit an immune response to more than one genospecies of Lyme disease causing strains of *Borrelia*, including genospecies and strains that are not used to generate the chimeric OspC immunogen.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a schematic diagram of the frequency distribution of major *ospC* groups among *B. burgdorferi* isolates from Eastern Long Island *Ixodes scapularis* ticks.

Figure 2 is a bar graph showing the reactivity of serum from mice immunized with the indicated *Borrelia* protein or recombinant chimeric *Borrelia* protein (X-axis) against the indicated OspC antigens (legend) where the serum is from the first bleed.

Figure 3 is a bar graph showing the reactivity of serum from mice immunized with the indicated *Borrelia* protein or recombinant chimeric *Borrelia* protein (X-axis) against the indicated OspC antigens (legend) where the serum is from the second bleed.

Figure 4 is a bar graph showing the reactivity of serum from mice immunized with the indicated *Borrelia* protein or chimeric recombinant *Borrelia* protein (X-axis) against the indicated strains of *Borrelia burgdorferi* sensu stricto (legend).

Figure 5 is a bar graph showing the reactivity of serum from mice immunized with the indicated *Borrelia* protein or chimeric recombinant *Borrelia* protein (X-axis) against the indicated strains of *Borrelia burgdorferi* sensu lato (legend).

Figure 6 is bar graph showing the reactivity of serum from mice immunized with the indicated *Borrelia* protein or chimeric recombinant *Borrelia* protein (X-axis) against the indicated strains of *Borrelia afzelii* (legend).

Figure 7 is bar graph showing the reactivity of serum from mice immunized with the indicated *Borrelia* protein or chimeric recombinant *Borrelia* protein (X-axis) against the indicated strains of *Borrelia garinii* (legend).

Figure 8 is a Table comparing the reactivity of lipidated OspC proteins C1 and C2 against sera from patients with the indicated condition with the reactivity of the unlipidated chimeric proteins of the present invention, where the number in parentheses is the total number of sera tested in that category.

DETAILED DESCRIPTION OF THE INVENTION

As described herein, initially nineteen groups of *ospC* from *B. burgdorferi* sensu stricto were found within a small tick population (Wang, I-N., *et al.*, *Genetics*, 151:15-30 (1999)). Major *ospC* groups were defined using the observation that *ospC* alleles are either very similar, having less than 2% sequence divergence, or very different, having greater than 8% sequence divergence, with most having greater than 14% sequence divergence.

Based on sequence divergences, alleles of *ospC* can be grouped into twenty-one major groups (Table II). To assess whether strain differences as defined by a given *ospC* group are linked to invasiveness and pathogenicity, the frequency distributions of major *ospC* groups from ticks, from the primary erythema migrans (EM) skin lesion,

and from secondary sites, principally from blood and spinal fluid, were compared. As described herein, the frequency distribution of *ospC* groups from ticks is significantly different from that of primary site infection which in turn is significantly different from secondary sites. The major *ospC* groups A, B, I and K increased in frequency from ticks to the primary site and were the only groups found in secondary sites of the infection. Therefore, three categories of major *ospC* groups are defined herein. One category is common in ticks but very rarely, if ever, causes human disease, a second category that causes only local infection at the tick bite site, and a third category that causes systemic or disseminated disease. While many *ospC* groups found in ticks were also found in primary skin lesions, the frequency distributions are significantly different between ticks and primary skin lesions (Table III). All *ospC* groups were found more or less commonly in ticks. However, only four groups are commonly found in skin lesions or secondary infections (Tables III and IV). As described herein, the primary skin lesions harbored *Borrelia* having *ospC* groups other than A, B, I or K rarely or not at all. More importantly, only these four *ospC* groups were found in secondary sites. The finding that all systemic *B. burgdorferi* sensu stricto infections are associated with four *ospC* groups has importance in the diagnosis, treatment and prevention of Lyme disease.

There is evidence that *ospC* has been transferred between strains and even between genospecies (Wang I-N, *et al.*, *Genetics*, 151:15-30 (1998)). This is not true of *Borrelia* chromosomal genes (Dykhuizen, D.E., *et al.*, *Proc. Natl. Acad. Sci.*, 30:10163-10167 (1999); Maynard Smith, J. and Smith, N.H., *Mol. Biol. Evol.*, 15:590-599 (1998)). However, *ospA* and *ospC* alleles in *B. Burgdorferi* sensu stricto are almost completely linked (Wang I-N, *et al.*, *Genetics*, 151:15-30 (1999)). This suggests that once an *ospC* allele has been transferred into a particular background, there is little or no selection for another similar recombination event. Thus, each major *ospC* group represents a clonal population descended from a single recombination.

Twenty percent of untreated erythema migrans clear spontaneously without causing any systemic complications (Steere, A.C. *et al.*, *Arth. Rheum.* 20:7-17, (1977)).

As demonstrated herein, this is not significantly different ($p = 0.25$ for a 2 by 2 contingency test with double dichotomy) from the percent of non-invasive strains found in the skin, suggesting that the erythema migrans that clear spontaneously are caused by non-invasive clones.

5 There is extensive genetic and antigenic diversity of *ospC* in all three pathogenic genospecies of *B. burgdorferi* sensu lato (Livey, I. *et al.*, *Mol. Microbiol.* 18:257-269, 1995; Masuzawa, T. *et al.*, *Clin. Diagn. Lab. Immunol.* 4:60-63, 1997; Picken, R.N. *et al.*, *J. Invest. Dermatol.* 110:211-214, 1998; Theisen, M. *et al.*, *J. Clin. Microbiol.* 31:2570-2576, 1993; Wang, I-N. *et al.*, *Genetics* 151:15-30 (1999). As demonstrated
10 herein, only four groups of *ospC* alleles are linked to both infectivity and invasiveness, and that invasiveness is confined to a small number of *ospC* clones. It is clear that the *ospA* and *ospC* alleles are tightly linked even though they are on different plasmids (Wang, I-N. *et al.*, *Genetics* 151:15-30 (1999)). If the invasiveness is caused by allelic variation at another locus, this variation is likely to be tightly linked to the *ospC*
15 variation. Thus, *ospC* is a good marker for human pathogenicity and perhaps its determinator. These findings have important implications not only for our understanding of the pathogenesis of this disease but for its diagnosis and prevention.

 Spirochetemia is a transient phenomenon, but is presumably key in seeding secondary skin sites, the heart, joints, and nervous system, where these *Borrelia* cause
20 the secondary and tertiary clinical manifestations of Lyme disease. All four invasive groups of *Borrelia burgdorferi* were found in isolates from blood and CSF. The one joint isolate belonged to group A. However, it can be inferred that groups not found in the blood will not be found in the joints since most if not all dissemination of *Borrelia* to secondary sites is via blood.

25 Normally, model organisms are used as substitutes for experiments on humans. However, this substitution works only as long as the properties of the model organism and of humans are the same for the studied phenomena. The human immune system plays a critical role which is expected to be different from the immune response in

model organisms, particularly the mouse. Humans are accidental and usually dead-end hosts while the mouse is a critical host reservoir. The field of population genetics has developed sound procedures for reaching conclusions from survey data.

The chimeric polypeptides of the present invention elicit specific immune
5 responses to OspC. The chimeric polypeptides also elicit immune response against strains of Lyme disease causing *Borrelia* of the same genospecies as that represented by the chimeric OspC as well as Lyme disease causing *Borrelia* of different genospecies than that represented by the chimeric OspC. The immune response includes humoral responses, secretory responses, cell-mediated responses and combinations thereof in an
10 animal treated with the compositions of the present invention. The compositions of the present invention can include additional components suitable for *in vitro* and *in vivo* use. These additional components include buffers, carrier proteins, adjuvants, preservatives and combinations thereof.

The immunogenic compositions of the present invention can be used to
15 immunize animals including humans. Immunization is understood to elicit specific immunogenic responses as described above. As described herein, an immunogenic response includes responses that result in at least some level of immunity in the treated animal, where the animal was treated with a composition comprising at least one protein or chimeric protein of the present invention. In one embodiment, the treated animal
20 develops immunity against infection by Lyme disease causing *Borrelia*, wherein the chimeric proteins of the present invention elicit responses against *Borrelia burgdorferi*, *Borrelia afzelii* and *Borrelia garinii*.

Immunity, as described herein, is understood to mean the ability of the treated animal to resist infection, to resist systemic infection, to overcome infection such as
25 systemic infection or to overcome infection such as systemic infection more easily or more quickly when compared to non-immunized or non-treated individuals. Immunity can also include an improved ability of the treated individual to sustain an infection with reduced or no clinical symptoms of systemic infection. The individual may be

treated with the chimeric proteins of the present invention either proactively, e.g. once a year or maybe treated after sustaining a tick bite.

For use as a vaccine, the composition of the present invention can include suitable adjuvants, well known in the art, to enhance immunogenicity, potency or half-life of the chimeric proteins in the treated animal. Adjuvants and their use are well known in the art (see for example PCT Publication WO 96/40290, the entire teachings of which are incorporated herein by reference). The composition can be prepared by known methods of preparing vaccines. For example, the OspC proteins or chimeric proteins to be used in the compositions can be isolated and/or purified by known techniques such as by size exclusion chromatography, affinity chromatography, preparative electrophoresis, selective precipitation or combinations thereof. The prepared proteins or chimeric proteins can be mixed with suitable other reagents as described above, where the chimeric protein is at a suitable concentration. The dosage of protein or chimeric protein will vary from one μg to 500 μg and depends upon the age, weight and/or physical condition of the animal to be treated. The optimal dosage can be determined by routine optimization techniques, using suitable animal models.

The composition to be used as a vaccine can be administered by any suitable technique. In one embodiment, administration is by injection, e.g. subcutaneous, intramuscular, intravenous, or intra peritoneal injection. In another embodiment, the composition is administered to mucosa, e.g. by exposing nasal mucosa to nose drops containing the proteins of chimeric proteins of the present invention. In another embodiment, the immunogenic composition is administered by oral administration. In another embodiment of the present invention the chimeric proteins are administered by DNA immunization.

Like many outer surface proteins of *Borrelia*, OspC is produced in the *Borrelia* spirochete with 5' lipidation. The chimeric polypeptides of the present invention can be produced in both lipidated and non-lipidated form. In one embodiment, the lipidation signal encoded by the wild type *ospC* is removed from the coding sequence, such that

the gene or chimeric gene encodes a non-lipidated OspC or chimeric OspC polypeptide. In another embodiment of the present invention, the lipidation signal of the wild type *ospC* gene is replaced with the lipidation signal of the *ospB* gene. In this embodiment, a lipidated OspC or OspC chimeric protein is produced.

5 The polypeptides of the present invention can be recombinantly expressed in suitable microbial hosts, wherein said hosts include, but are not limited to, bacterial hosts, such as *E. coli*, fungal hosts *S. cerevisiae*, or cell culture hosts such as mammalian cell culture or insect cell culture.

 While the lack of lipidation signal allows for the production of large amounts of
10 OspC proteins and chimeric OspC proteins, the lack of lipidation signal was previously thought to render outer surface proteins of *Borrelia* less or non-immunogenic. However, as described herein, the non lipidated chimeric polypeptides of the present invention unexpectedly elicit as broad an immunogenicity as lipidated OspC protein (Figures 2 and 3) and greater immunogenicity against strains of other genospecies
15 (Figure 5-7) compared to the positive controls, which were lipidated OspC from B31 and lipidated OspC from C12.

 The proteins and chimeric proteins of the present invention are also antigenic and therefore useful to detect or diagnose the presence of Lyme disease causing *Borrelia*, especially *Borrelia* from groups capable of causing disseminated symptoms of
20 Lyme disease. As described herein, disseminated symptoms refers to infection outside of the erythema migrans skin lesion, e.g. infection in blood, CNS or synovia. As described herein, antigenic refers to the ability of a compound to bind products of an immune response, such as antibodies, T-cell receptors or both. Such responses can be measured using standard antibody detection assays, such as ELISA or standard T-cell
25 activation assays.

 The present invention is drawn to compositions comprising OspC polypeptides from Lyme disease causing *Borrelia* and chimeric OspC polypeptides. In one embodiment of the present invention, compositions include one or more OspC

polypeptide or fragment thereof from at least two *Borrelia burgdorferi ospC* groups, referred also herein as families, selected from the group consisting of A, B, I and K, excepting the combination consisting of two *OspC* polypeptides from the A and I families. In another embodiment of the present invention, the compositions of the present invention include at least one *OspC* polypeptide or fragment thereof from each of *Borrelia burgdorferi ospC* families A, B, I and K. In another embodiment, the composition includes at least one *OspC* polypeptide or fragment thereof from each of *Borrelia afzelii* *OspC* families A and B. In still another embodiment, the composition includes *OspC* polypeptides from at least one *Borrelia burgdorferi* *OspC* group or family member selected from the group consisting of A, B, I and K and at least one *Borrelia afzelii* *OspC* family member selected from the group consisting of A and B.

As described herein, the *ospC* families of the present invention share about 98% homology at the nucleic acid level between strains of the same family and share no more than about 92% homology at the nucleic acid level between strains of different families. Determination of homology excludes any non-*ospC* sequences. Members of the same *ospC* family have similar antigenic profiles, e.g. elicit immune response against similar strains of Lyme disease causing *Borrelia*. The chimeric proteins of the present invention unexpectedly elicit immune response to Lyme disease causing *Borrelia* of different genospecies than the genospecies from which the component polypeptides were derived. In one embodiment of the present invention, *Borrelia burgdorferi ospC* family A comprises strains B31, CA4, HII, IPI, IP2, IP3, L5, PIF, PKA, TXGW and strains of *Borrelia* containing *ospC* allele OC1. In another embodiment of the present invention, *Borrelia burgdorferi ospC* family B comprises strains 35B808, 61BV3, BUR, DK7, PB3, ZS7 and strains containing *ospC* alleles OC2 and OC3. In still another embodiment of the present invention, *Borrelia burgdorferi ospC* family I comprises strains 297, HB19 and strains containing *ospC* allele OC10, wherein strain 297 is characterized by *ospC* of GenBank Accession No. L42893. In still another embodiment of the present invention, *Borrelia burgdorferi ospC* family K

comprises strains 272, 297, 28354, KIPP, MUL and strains containing *ospC* allele OC12 and OC13, wherein strain 297 is characterized by *ospC* of GenBank Accession No. U08284.

In another embodiment of the present invention, said compositions comprise an
5 *OspC* polypeptide or fragment thereof from each of *Borrelia afzelii* *OspC* families A and B. In one embodiment of the present invention, *Borrelia afzelii* *OspC* family A comprises strains Pbo, Pwud, Pko, Pgau, DK2, DK3, DK21, DK8, Bfox and JSB. In another embodiment of the present invention *Borrelia afzelii* *OspC* family B comprises strains DK5, ACA1, DK9, XB18h, Ple and 143M. As described above for *Borrelia*
10 *burgdorferi* the compositions also include chimeric *OspC* polypeptides of *Borrelia afzelii* families A and B.

In one embodiment of the present invention, the *OspC* polypeptide *OspC* polypeptide is a chimeric *OspC* comprising at least one *OspC* protein variable region or portion thereof from at least one *ospC* gene. In one embodiment of the present
15 invention, the *OspC* polypeptide variable region is encoded by a nucleic acid comprising the 3' two thirds of the *OspC* gene, about nucleotide 150 to about nucleotide 519 of an *ospC* gene (or about codon 50 to about codon 173). In another embodiment of the present invention, said *OspC* polypeptide variable region is encoded by a nucleic acid wherein the nucleic acid comprises, for example, nucleotide 244 to
20 about nucleotide 519 (or about codon 81 to about codon 173), nucleic acid from about nucleotide 337 to about nucleotide 519 (or about codon 112 to about codon 173), nucleic acid from about nucleotide 418 to about nucleotide 519 (or about codon 139 to about codon 173), nucleic acid from about nucleotide 244 to about nucleotide 418 (or about codon 81 to about codon 139), nucleic acid from about nucleotide 337 to about
25 nucleotide 418 (or about codon 112 to about codon 139), and nucleic acid from about nucleotide 150 to about nucleotide 243 (or about codon 50 to about codon 81) of an *ospC* gene.

In still another embodiment, the chimeric OspC polypeptides of the present invention comprises two or more polypeptides wherein a first polypeptide is from a first *ospC* gene from about nucleotide 26 (or about codon 8) to about nucleotide 630 (or about codon 210). In another embodiment, the first polypeptide is from about
5 nucleotide 28. In another embodiment, the first polypeptide is from about nucleotide 53. In still another embodiment, the first polypeptide is from about nucleotide 55. In another embodiment, the first polypeptide is up to about nucleotide 621 of a first *ospC* gene. In still another embodiment, the first polypeptide is up to about nucleotide 582 of a first *ospC* gene. In still another embodiment, the first polypeptide is up to about
10 nucleotide 576 of a first *ospC* gene.

The chimeric OspC of the present invention further comprises a second polypeptide, wherein the second polypeptide is derived from a second *ospC* gene from about nucleotide 28 (or about codon 9) to about nucleotide 571 (or about codon 190).

It is understood that the polypeptides than comprise the chimeric polypeptide
15 can include extra nucleotides or fewer nucleotides from the given *ospC* gene from which the polypeptide is derived in order to simplify the construction of the gene encoding the chimeric polypeptide, e.g. to allow for the use of convenient restriction endonuclease sites or to allow the ligation of the gene fragments such that a contiguous coding region is created. Based on the guidance provided herein, one of ordinary skill
20 in the art would readily be able to add or remove nucleotides from the termini of the gene fragments encoding the polypeptides of the chimeric OspC protein to generate chimeric proteins of the present invention with no or only routine experimentation. Furthermore, there can be an extra about 1 to about 10 amino acids on the N- and/or C-terminus of the polypeptides and chimeric proteins of the present invention and still
25 retain the properties of the present invention.

The present invention also includes variants or altered versions of the OspC polypeptides and nucleic acids encoding said polypeptides. As used herein, a variant of a polynucleotide or polypeptide refers to a molecule that is substantially similar to

either the entire molecule, or a fragment thereof. For example, when the molecule is a polypeptide, variant refers to an amino acid sequence that is altered by one or more amino acids, wherein either a biological function, structure or antigenicity of said sequence or combination thereof is maintained in the variant. The variant may have

5 “conservative” changes, wherein a substituted amino acid has similar structural or chemical properties, *e.g.*, replacement of leucine with isoleucine. Or a variant may have “nonconservative” changes, *e.g.*, replacement of a glycine with a tryptophan. Similar minor variations may also include amino acid deletions or insertions, or both.

Similarly, when the molecule is a polynucleotide, variant refers to a sequence that is

10 altered by one or more nucleotides. The variant may have silent variations, wherein the change does not alter the amino acid encoded by the triplet comprising said variation or the variation is not silent, that is, alterations in encoded amino acids are generated.

As used herein, the term “altered version” refers to a polynucleotide sequence or a polypeptide sequence, wherein said sequence has one or more differences with a

15 native or wildtype version of said sequence.

In another embodiment, the invention includes an isolated nucleic acid molecule comprising a nucleotide sequence which is homologous to one or more of the chimeric sequences of the present invention, or complements thereof. Such a nucleotide sequence exhibits at least about 80% homology, or sequence identity, with one of the

20 chimeric *OspC* sequences, such that the encoded protein retains the antigenicity and immunogenicity of the unaltered chimeric protein. Preferably, the homologous sequences of the present invention shares at least about 90% homology or sequence identity with the corresponding unaltered chimeric *ospC*. Particularly preferred sequences have at least about 95% homology or have essentially the same sequence.

25 The altered nucleic acids and homologous nucleic acids of the present invention hybridize to the corresponding chimeric *ospC* under conditions of high stringency. A general description of stringency for hybridization conditions is provided by Ausubel, F.M., *et al.*, *Current Protocols in Molecular Biology*, Greene Publishing Assoc. and

Wiley-Interscience 1987, & Supp. 49, 2000. Factors such as probe length, base composition, percent mismatch between the hybridizing sequences, temperature and ionic strength influence the stability of nucleic acid hybrids. Thus, stringency conditions, sufficient to allow hybridization of oligonucleotides to the template, can be
5 varied by routine optimization to generate high stringency conditions.

Alternatively, conditions for stringency are as described in WO 98/40404, the teachings of which are incorporated herein by reference. In particular, examples of highly stringent, stringent, reduced and least stringent conditions are provided in WO 98/40404 in the Table on page 36. Examples of stringency conditions are shown in
10 Table I below which is from WO98/40404 to Jacobs *et al.*; highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

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Table 1

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [‡]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
5	A	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	<50	T _B *; 1xSSC	T _B *; 1xSSC
	C	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	<50	T _D *; 1xSSC	T _D *; 1xSSC
	E	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
10	F	<50	T _F *; 1xSSC	T _F *; 1xSSC
	G	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	<50	T _H *; 4xSSC	T _H *; 4xSSC
	I	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	<50	T _J *; 4xSSC	T _J *; 4xSSC
15	K	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	<50	T _L *; 2xSSC	T _L *; 2xSSC
	M	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	<50	T _N *; 6xSSC	T _N *; 6xSSC
	O	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
20	P	<50	T _P *; 6xSSC	T _P *; 6xSSC
	Q	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	<50	T _R *; 4xSSC	T _R *; 4xSSC

‡: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides.

When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

†: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length

should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C) = 81.5 + 16.6(log₁₀[Na⁺]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1xSSC = 0.165 M).

As used herein, “isolated” refers to nucleic acid or polypeptide that has been removed from its original environment (*e.g.*, the natural environment if it is naturally occurring). For example, polynucleotide or DNA or polypeptide, which is separated from some or all of the coexisting materials in the natural system. An isolated polynucleotide can be part of a vector and/or composition, and still be isolated in that the vector or composition is not part of its natural environment. Likewise polypeptides can be part of a composition and still be isolated in that the composition is not part of its natural environment.

The chimeric proteins of the present invention comprise OspC proteins or polypeptides as described above from two or more OspC families of Lyme disease causing *Borrelia* as described in Table II. In one embodiment of the present invention, said families comprise *Borrelia burgdorferi* OspC families A, B, I and K and *Borrelia afzelii* OspC families A and B. The chimeric proteins of the present invention comprise, for example, a first OspC polypeptide encoded by a nucleic acid comprising a sequence from about codon 18 to about codon 210 of a first *ospC* gene. In another embodiment,

the sequence is from about codon 8. In another embodiment, the sequence is to about codon 207. In another embodiment, the sequence is to about codon 194. In still another embodiment, the sequence is to about codon 192. The chimeric proteins of the present invention further comprise, for example, a second OspC polypeptide comprising an

- 5 OspC variable polypeptide encoded by nucleic acid fragments as described above. In another embodiment of the present invention, the chimeric protein comprises two or more OspC variable polypeptides as described above.

- The chimeric proteins of the present invention further comprise, for example, a second OspC polypeptide encoded by a nucleic acid comprising a sequence from about
10 codon 9 to about codon 190 of a second *ospC* gene.

- For the chimeric proteins of the present invention, at least two of said OspC polypeptides or immunogenic fragments thereof are fused together in a single protein, a chimeric protein, encoded by a single nucleic acid, wherein no two adjacent polypeptides in said fusion protein are found in the same configuration in a naturally occurring OspC
15 protein.

In still another embodiment, the OspC proteins or chimeric proteins of the present invention from *Borrelia burgdorferi* and *Borrelia afzelii* are combined in a composition.

- The present invention is drawn to a method of detecting an immune response to
20 Lyme Disease causing *Borrelia* in a host sample. The method comprises contacting the host sample with a composition comprising OspC polypeptides from Lyme disease causing strains of *Borrelia*, such that anti-OspC antibodies, if present, in said sample bind to said OspC polypeptides. In one embodiment, the composition comprises one or more OspC polypeptide or diagnostic fragment thereof from two *Borrelia burgdorferi*
25 OspC families selected from the group consisting of A, B, I and K, excluding the composition consisting of two OspC proteins wherein one OspC protein is from OspC family A and the second OspC protein is from OspC family I. The antibodies that bind the OspC polypeptides of the composition are detected or measured; thereby detecting an

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immune response to Lyme disease causing *Borrelia*. In another embodiment, the composition comprises at least two *Borrelia* OspC polypeptides or diagnostic fragment thereof from two *Borrelia afzelii* OspC families selected from the group consisting of A and B. In still another embodiment, the composition comprises polypeptides from OspC
5 from *Borrelia burgdorferi* and *Borrelia afzelii*. In still another embodiment, the composition comprises one or more polypeptides from each of *Borrelia burgdorferi* families A, B, I and K and *Borrelia afzelii* families A and B. The composition can also comprise one or more of the chimeric polypeptides of the present invention.

The present invention is also drawn to kits comprising one or more OspC
10 polypeptides or OspC chimeric polypeptides or combinations thereof together with suitable buffers and antibody detection reagents for the detection or diagnosis of Lyme disease causing strain of *Borrelia*. In another embodiment, the kits comprise nucleic acid sufficiently homologous to the OspC polypeptides or OspC chimeric polypeptides to detect nucleic acid encoding *ospC* genes from Lyme disease causing strains of
15 *Borrelia* together with reagents to detect positive hybridization to target DNA or reagents to specifically DNA, for example.

For the purposes of a detection kit, "homologous" refers to two or more sequences that share substantial similarity but are not identical. Two DNA sequences are "substantially similar" when at least about 95% (preferably at least about 98%) of the
20 nucleotides match over a defined length of the DNA sequences. Sequences that are substantially homologous can be identified by comparing the sequences using standard software available in sequence data banks, or in a Southern hybridization experiment under, for example, stringent conditions as defined for that particular system. Defining appropriate hybridization conditions is within the skill of the art. See, *e.g.*, Ausubel *et*
25 *al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, Inc., New York; Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press. For purposes of the present invention, amino acid sequences having, for example, greater than 90 percent similarity are considered substantially homologous.

The vaccine compositions of the present invention elicit humoral and cell mediated immune responses in a host. Furthermore, the diagnostic compositions of the present invention are capable of detecting both humoral and cell mediated immune response from a host sample using standard immunodiagnostic techniques.

5

EXEMPLIFICATION

EXAMPLE 1: - TECHNIQUES

Borrelia strains

One hundred and forty *B. burgdorferi* strains were isolated from primary erythema migrans (EM) lesions, blood or cerebrospinal fluid (CSF) of patients seen at the Lyme Disease Center at Stony Brook, New York, Lyme Disease Diagnostic Center at New York Medical College, Valhalla, New York or the private practices of the two collaborating physicians on the eastern end of Long Island or were obtained from the Centers for Disease Control (CDC). All patients met the Centers for Disease Control surveillance definition for Lyme Disease (CDC, *Morb. Mortal. Wkly. Rep.* 46:20-21, (1997)). Isolates from skin, blood and CSF were obtained using standard techniques (Barbour, A.G., *Yale J. Biol. Med.* 57:521-525, 1984; Berger, B.W. *et al.*, *J. Clin. Microbiol.* 30:359-361, 1992; Wormser, G.P. *et al.*, *J. Clin. Microbiol.* 36:296-298, (1998)). Punch biopsies were taken from the advancing border of the erythema migrans lesion and incubated in BSK-H medium (Sigma, St. Louis, MO) at 34°C to create a culture. There was little culture bias as determined by direct analysis of biopsy tissue compared to culture isolates (Seinost, G. *et al.*, *Arch. Derm.*, 135:1329-1333, (1999)), unlike isolation of *B. burgdorferi* from unfed ticks (Norris, D.E. *et al.*, *J. Clin. Microbiol.* 35:2359-2364, (1997)). In addition, twenty-two *B. burgdorferi sensu stricto* *ospC* sequences were retrieved from GenBank. The tick data used was either from GenBank or from the study of Wang *et al.* (Wang, I-N. *et al.*, *Genetics* 151:15-30 (1999)).

DNA isolation

For isolation of genomic *Borrelia* DNA, log phase cells were harvested by centrifugation at 10,000 RPM for 30 minutes at 4°C. The bacterial pellet was resuspended in Tris/saline-buffer (10 mM Tris (pH 7.5), 150 mM NaCl). The bacteria
 5 were then pelleted and resuspended in TNE (10 mM Tris (pH 7.5) 150 mM NaCl, 1 mM EDTA). Freshly prepared lysozyme (20 mg/ml in TNE), sodium dodecyl sulfate (10%) and proteinase K (20 mg/ml) were added and the mixture was incubated at 50°C for one hour, followed by RNase treatment. DNA was extracted with phenol/chloroform, precipitated with ethanol and resuspended in TE buffer.

10 Polymerase chain reaction

The *ospC* gene was amplified using PCR, as described previously (Wang, I-N. *et al.*, *Genetics* 151:15-30 (1999)). The *OspC* gene was amplified using two external primers: 5'-AAA GAA TAC ATT AAG TGC GAT ATT-3' (+), SEQ ID NO: 1, beginning at base 6; and 5'-GGG CTT GTA AGC TCT TTA ACT G-3' (-), SEQ ID NO:
 15 4, ending at base 602. The 5' half of *ospC* was amplified using SEQ ID NO: 1 and the reverse primer, 5'-CAA TCC ACT TAA TTT TTG TGT TAT TAG-3' (-) SEQ ID NO: 2; ending at base 345. The 3' half of *ospC* was amplified using the primer, 5'-TTG TTA GCA GGA GCT TAT GCA ATA TC-3' (+), SEQ ID NO: 3, beginning at base 289, and SEQ ID NO: 4 as the reverse primer. The external primers amplified a 597 bp fragment.
 20 Amplification of the 5' half produced a 340 bp fragment while amplification of the 3' half produced a 314 bp fragment. All the base numbers and amplified fragment sizes are based on *ospC* sequence of strain B31 (GenBank accession number U01894), with start codon as base 1.

Amplification was conducted in 50µl of a solution containing Perkin-Elmer
 25 Cetus 10x PCR buffer (100 mM Tris-HCl (pH 8.3), 500 mM KCl), 2.5 mM MgCl₂, deoxynucleoside triphosphates at 0.2 mM per nucleotide, 2.5 U of Taq polymerase (Perkin-Elmer/Cetus) and 0.5 µM of each primer. The amplification reaction was

carried out for forty cycles in a DNA thermal-cycler (PTC-100; MJ Research, Inc., Watertown, MA) with an amplification profile of: denaturation at 95°C for 40 seconds, annealing at 54°C for 35 seconds, and extension at 72°C for 1 min, after an initial denaturation step at 96°C for 2 min. Negative controls were included in each experiment
5 to control for contamination.

Cold SSCP-analysis.

SSCP analysis was chosen to characterize genetic variation of the isolated *ospC* gene fragments based on its exquisitely high detection rate of DNA polymorphisms and point mutations at a variety of positions in DNA fragments (Orita, M. *et al.*, *Proc. Natl. Acad. Sci.* 86:2766-2770, (1989)). Single point mutations have been detected in
10 fragments up to 800bp long (Michaud, J. *et al.*, *Genomics*. 13:389-394, (1992)). However, there is evidence that the ability of SSCP analysis to detect mutations begins to decline significantly as PCR fragments approach 400bp in size (Hayashi, K., *PCR Methods & Applications* 1:34-38, (1991)). Therefore, in order to achieve high efficiency
15 of detection of nucleotide polymorphism, the length of the PCR products used herein was 340bp from the 5' half and 314bp from the 3' half of *ospC*.

Amplified *ospC* gene fragments from all one hundred and forty strains were analyzed for genetic variations by the cold SSCP protocol described by Hongyo *et al.* (Hongyo, T. *et al.*, *Nucleic. Acids Res.* 21:3637-3642, (1993)). Briefly, 5 to 15 µl of the
20 PCR product was added to a mixture containing 4 µl 5x TBE Ficoll sample Buffer (NOVEX, San Diego, CA) and 0.4 µl 1 µM methylmercury hydroxide (Alfa Aesaer, Ward Hill, MA). The amount of the PCR product used for the SSCP analysis was estimated after visualizing the PCR product on an agarose gel with ethidium bromide. The sample mixture was heated to 95°C for 4 min, then chilled on ice prior to loading
25 the entire 20 µl into the gel sample well. The sharpest bands were observed when the sample was applied to a pre-cast 20% TBE gel (NOVEX) electrophoresis system (ThermoFlow ETC Unit, NOVEX) with 1.25x TBE running buffer. Electrophoresis of

SSCP products was conducted at a constant temperature of 8°C for 17 h at 240 volts in order to reveal discernable mobility shifts. Gels were stained with 0.5 µl/ml ethidium bromide in 1x TBE buffer for 25 min and destained in distilled water for 30 min.

- Stained bands were viewed using a 340nm UV staining box. Samples that showed more
 5 than two SSCP bands were reamplified to determine whether the bands found were real alleles or the product of PCR artifacts. Side-by-side SSCP analysis was performed in order to detect even slight shifts in electrophoretic mobility.

DNA sequencing

The *ospC* gene or representatives of each mobility class were reamplified.

- 10 Double-stranded PCR fragments were purified by agarose gel electrophoresis and subjected to automated DNA sequencing using fluorescent dideoxy terminator chemistry and the forward and reverse primers originally used for PCR amplification.

Statistical analysis

- Chi square analysis of contingency tables was performed. This analysis tests for
 15 significant difference in frequency distributions. The tables were 2xN where N is the number of major *ospC* groups distinguished. The average expected number in each element of the table needs to be about six or greater for an unbiased test (Zar, J.H., *Biostatistical Analysis*, 3rd ed, p. 206, (1996)). This means that the number of observations should be greater than 6 times 2N. When the expected average number was
 20 less than six, the major *ospC* groups with the lowest number in the sample were combined until the number of observations were about equal to or greater than 12N.

RESULTS

ospC mobility classes in human *B. burgdorferi* isolates.

- One hundred and thirty-two isolates of *B. burgdorferi* sensu stricto from patient
 25 samples of skin, blood, and CSF (Table II) were propagated *in vitro* and used as a source

of DNA for analysis. The *ospC* genotype of each strain was determined by cold SSCP analysis of the 5' end (340bp) of the gene and was confirmed by SSCP analysis of the 3' end (314bp) of *ospC*. In all *B. burgdorferi* isolates, the genetic variation at the 5' end of the gene corresponded to the variation at the 3' end. At least two representatives of each

5 SSCP mobility class were subsequently sequenced. The sequences of the same mobility classes were identical in all samples and each mobility class had a unique sequence. Therefore, the sensitivity and specificity of SSCP analysis was 100%. Each SSCP mobility class was designated as an allele. Wang *et al.* recently described 13 *ospC* alleles (Wang, I-N. *et al.*, *Genetics* 151:15-30). An additional five *ospC* (OC) mobility

10 classes, OC14-18 are described herein. OC14 has the same *ospC* sequence as the *ospC* in strain 2591.

TABLE II. Alignment of major *ospC* groups with *ospC* alleles identified by SSCP analysis

	Major <i>ospC</i>	<i>ospC</i> allele	GenBank			Dis-
	Group	(SSCP)	number ¹	Ticks	Skin ²	seminated ²
5	A	1	AF029860	17	23	21
	B	2	AF029861	17	19	4
	C	3	AF029862	11	3	0
	D	4	AF029863	10	1	0
	E	5, 7	AF029864	6	1	0
10	F	6	AF029865	9	0	0
	G	8	AF029867	5	7	0
	H	9	AF029868	7	6	0
	I	10	AF029869	1	9	3
	J	11, 18	AF029870	3	7	0
15	K	12, 13	AF029871	6	32	16
	L	-	L42899	2	0	0
	M	14	U01892	1	3	0
	N	15	L42899	1	3	0
	O	-	X84778	0	1	0
20	P	-	U91796	1	0	0
	Q	-	U91790	1	0	0
	R	-	U91791	2	0	0
	S	-	U91793	1	0	0
	T	16	AF065143	0	1	0
25	U	17	AF065144	0	2	0

¹ A single GenBank sequence of each type is given as an example.

² The number of each major *ospC* group observed in blood, synovial fluid or cerebrospinal fluid. This includes both SSCP data and data from the literature, including GenBank.

- 5 **B. burgdorferi* sensu stricto Groups P through S are only found in Europe. Groups R and S are excluded from the analysis because nearly identical *ospC* alleles are found in *B. afzelii* and *B. garinii*, showing these groups were recently created by cross-species transfer.

10 Multiple infections

Of the one hundred and thirty-two primary isolates from patients with Lyme disease in this study, most contained only a single strain. Seven skin isolates and one CSF isolate contained two different strains as determined by SSCP analysis, thus giving a total of one hundred and forty different strains. The *ospC* allele pairs found in

15 multiply infected erythema migrans biopsy specimens were (OC1, OC12), (OC1, OC14), 2x(OC2, OC3), 2x(OC2, OC12), and (OC8, OC18). CSF isolate NY940657 contained *ospC* alleles OC1 and OC12. For CSF isolate 297, which was isolated in Connecticut, there were two *ospC* sequences published in GenBank: L42893, which is analogous to OC10 and U08284, which is analogous to OC12. The pair-wise difference

20 of *ospC* sequences of both strains is 16.4%, suggesting CNS infection with two different strains in this isolate. Overall, 5.5% of all isolates described herein contained two strains. Because as many as 50% of ticks isolated in the wild are infected with multiple strains, exposure to multiple strains in a single tick bite is common, raising the possibility that different strains are differentially pathogenic.

- 25 To these one hundred forty strains for which the *ospC* allele was determined herein, twenty-two strains of known *ospC* sequence from GenBank were added to give a total of one hundred sixty-two. Fifty-one of these strains were obtained either from

eastern Long Island; seventy-seven were obtained from Westchester County, New York, and the remainder from other endemic areas in the United States (twenty-two strains) and Europe (twelve strains). The isolates were divided into those from the site of the primary infection, the erythema migrans skin lesion (one hundred eighteen isolates), and those from secondary sites, where the infection had disseminated (forty-four isolates). This later group included, for example, twenty from cerebro-spinal fluid (CSF), twenty-three from blood, and one from synovial fluid.

Major *ospC* groups in human *B. burgdorferi* isolates

Surprisingly, as described herein, the differences between *ospC* sequences among and between the families of *B. burgdorferi* sensu stricto fell into two groups. Pairs of *ospC* genes within the same family differed in nucleic acid sequence by less than two percent while pairs of *ospC* genes from separate families in nucleic acid sequence differed by more than eight percent. Wang *et al.*, defined nineteen major *ospC* groups, designated A to S (Wang, I-N. *et al.*, *Genetics* 151:15-30 (1999)). As described herein, two additional *ospC* groups are provided, designated T and U. OC16 represents major group T and OC17 represents major group U (Table I). The lowest pair-wise differences of group T and U to any other major *ospC* group are 16.1% and 20.5% respectively.

B. burgdorferi clones are differentially pathogenic

As described herein, clones representing different *ospC* groups of *Borrelia burgdorferi* are differentially pathogenic. This is demonstrated by the differing frequencies of the various major *ospC* groups in ticks, in the initial infection in the skin, and in disseminated infections.

The strains in GenBank and the literature for which the *ospC* sequences have been determined were widely sampled from the entire geographic range of the species and were chosen irrespective of whether they were from ticks or humans. These strains

gave a small but random sample of the frequencies of the major *ospC* groups in ticks and humans. As demonstrated herein, the frequency of the major *ospC* groups from human isolates was found to be significantly different from the frequency found in ticks on Long Island. Table III shows that the frequency distribution of strains from skin
5 from eastern Long Island differ significantly from tick strains collected in the same area.

TABLE III

Major <i>ospC</i> groups	A	B	C	D	F	G	H	I	K	Comb. ^a
Isolates From										
Erythema migrans	13	6	2	0	0	1	0	4	16	4
10 lesions (N=46)										
Ixodes scapularis	12	12	11	9	6	5	7	1	5	6
ticks (N=74)										

$\chi^2 = 36.3$ with 9 degrees of freedom
 $p < 0.001$

^a Combined major groups are defined by individual frequencies of 0.025 or less and include groups E, J, N, O.

15 The analysis provided herein of all *ospC* groups presented in this study showed that most groups are found in both ticks and in humans (Table II). However, major groups A, B, I and K predominated in humans, with A and K groups found most frequently. (Figure 1).

The pattern of pathogenicity of the various clones as demonstrated by frequency
20 in the primary site of infection, the skin, compared to the frequency in secondary sites revealed that only four major groups (A, B, I and K) were found in both the skin and secondary sites (compare Tables III and IV). All other major groups were found only in the skin. When all groups with three or fewer isolates are combined to give the

combined group of Table IV, a 2 by 8 contingency test comparing the frequency distribution of skin versus secondary sites gives a significance of $p < 0.005$. When no groups are combined, a 2 by 15 contingency test is still significant ($\chi^2 = 24.07$ with 14 degrees of freedom, $p < 0.05$). The distribution of strains from primary and secondary sites indicated that only a certain of the major groups, A, B, I, and K cause disseminated disease. As described herein, these are referred to as invasive clones whereas other clones are referred to as non-invasive clones.

TABLE IV

Major <i>ospC</i> groups	A	B	G	H	I	J	K	Comb. ^a
10 Isolates From								
Erythema migrans	23	19	7	6	9	7	32	16
lesions (N=118)								
Disseminated Infections	21	4	0	0	3	0	16	0
(N=44)								

$\chi^2 = 23.6$ with 7 degrees of freedom
 $p < 0.005$

15 ^a Combined major groups are defined by individual frequencies of 0.025 or less and include groups C, D, E, M, N, O, T and U.

As described herein, the different clones of *B. burgdorferi* sensu stricto, as defined by *ospC* groups, are differentially pathogenic. Some groups very rarely, if ever, cause human disease, e.g. *ospC* groups D, E, F, and L. Some groups cause a local infection at the tick bite site, but not systemic disease, e.g. *ospC* groups G, H, J, and T. Finally, there are some groups which are responsible for systemic disease; these are

ospC groups A, B, I, and K. Our findings indicate that all systemic *B. burgdorferi* sensu stricto infections in humans are caused by strains in these four *ospC* groups.

Figure 1 shows the frequency distribution of major *ospC* groups among *B. burgdorferi* isolates from Eastern Long Island *Ixodes scapularis* ticks, n=72, (A); erythema migrans lesions, n=118, (B); and secondary sites of infection, n=44, (C). The percentage of group A plus K increased from 23% in the tick isolates, to 47% in the skin isolates, and to 84% in the secondary sites. The length of the bars in Figure 1 reflect this increase, by holding the length of the combined A and K groups constant. In the skin, groups C, D, E, M, N, O, T and U have been combined since their individual frequencies are 0.025 or less. This combination of groups when combined make up 12.7% of the total number of strains.

A similar analysis was conducted for *Borrelia afzelii*. The analysis included *OspC* alleles from 21 strains from GenBank and 12 strains sequenced for this study. These sequences fell into 20 major groups where the definition of a group is less than 1% sequence diversity within a group and at least 7.7% sequence difference between groups. There were two exceptions to this rule which were caused by a deletion in one *ospC* gene and a cross-species transfer of a small section of DNA in another *ospC* gene. When these anomalous sections were removed, all *ospC* alleles fell into 20 groups. Only two groups contained strains from chronic infections - groups A and B. By analogy and the *B. burgdorferi* study, it appears that only two groups are pathogenic in *B. afzelii*.

EXAMPLE 2: Protein Expression and Immunoblot

Protein Expression

The *Escherichia coli* (strain BL21 (pLysS) or strain B834 (DE3)) were transformed with the plasmid encoding the recombinant chimeric *Borrelia* proteins (RCBPs), and grown in 10 ml LB media (5 g/l NaCl, 10 g/l tryptone, 5 g/l yeast extract, 25 mg/l chloramphenicol and 50 mg/l ampicillin) at 37°C, with shaking. When the

optical density at 600λ reached 0.3-0.4 units, recombinant protein expression was induced by adding IPTG (isopropyl B-D-thiogalactopyranoside) to a final concentration of 0.5 mM and the cells were grown for an additional three hours. The cultures were harvested by centrifugation at 3800xg for five minutes. The cells were resuspended in 20 mM NaPO₄, pH7.7 and stored at -20°C overnight. Once thawed, the crude extracts were incubated with DNase (2 µg/ml) in the presence of 2.5 mM of MgCl₂ at room temperature for thirty minutes, spun at 14000 rpm (Eppendorf 5417C) for five minutes and 5 µl of the protein sample was run on a SDS-PAGE which was either stained in Commassie Blue or used for Immunoblot. Protein samples were solubilized, usually with a sodium dodecyl sulphate (SDS) containing buffer and in selected cases with reducing agents such as dithiothreitol (DTT) or 2-mercaptoethanol (2-ME). Following solubilization, the material was separated by SDS-PAGE. The proteins were then eletrophoretically transferred to a polyvinylidene difluoride membrane (PVDF, Immobilon-P®, Millipore). The transfer of proteins was monitored by a reversible staining procedure, Ponceau S. The stained membrane was made and the membrane destained by soaking in water for 10 minutes. All non-specific binding sites in the proteins and on the membrane were blocked by immersing the membrane in a solution containing a protein or detergent blocking agent (5 % milk in tris-buffered saline (TBS) Tween-20® 0.1%). The membranes were then incubated with primary antibody (either a monoclonal antibody or Erythema Migrans Lyme disease human serum). The membrane was washed and the antibody-antigen complexes were identified using alkaline phosphatase (AP) enzymes coupled to secondary antibody, either anti-immunoglobulin G (anti-mouse IgG) to detect the monoclonal antibody or anti-human IgA+IgG+IgM to detect the serum antibodies. A chromogenic substrate for alkaline phosphatase was then used to visualize the activity.

EXAMPLE 3: SEROLOGIC CHARACTERIZATION - ELISA (Enzyme-Linked Immunosorbent Assay)

Immobilization of RCBPs onto ELISA Plates, Determining Optimal RCBP Binding:

- 5 A solution of purified RCBPs in sodium phosphate buffer, pH 9.0 was used to coat commercial microwell plates (MaxiSorp®, Nunc). Recombinant OspC *Borrelia* proteins are described in Table V. The coating procedure was as follows: 100 µl of a solution containing the appropriate concentration of each RCBP was added to each well and the microwell plate was incubated for either one hour at room temperature or at 4°C
- 10 overnight. The antigen solution was removed from the wells, the plate washed three times with phosphate buffered saline (PBS) pH 9.0, and 200 µl of blocking solution added (2% BSA fraction V (Sigma) in PBS). Following a thirty minute incubation at 37°C, the plates were washed three times with PBS, wrapped in plastic and stored at 4°C until used. The binding of the individual RCBPs was measured using monoclonal
- 15 antibodies specific for either OspA or OspC followed (after washing) by an alkaline phosphatase-conjugated goat anti-mouse secondary antibody. The upper limit of protein binding was found to be beyond the working range of the monoclonal antibody used to measure it, and the standard blocking protocol was found to successfully saturate this high protein binding capacity, leaving low background readings in the
- 20 control wells. The results of these experiments indicated that a protein concentration of 0.5 µg/ml in the coating buffer was optimal for each of the RCBP tested. It was not found to be necessary that the chimeric proteins be immobilized in a specific molar ratio to one another; only that enough of each protein be bound so that epitopes in that chimeric protein do not become limiting in subsequent ELISA assays using patient
- 25 serum. For practical purposes, it was found that these conditions were met when the monoclonal-capture assay reached an absorbance of about 1.5 units or greater for each mouse monoclonal antibody, with a specific epitope represented in one of the chimeric proteins on the well surface. If necessary, however, the concentrations of individual

proteins in the mixture can be adjusted to achieve the desired levels of immobilized protein using routine optimization. Although the amount of each RCBP bound to the surface of the well and the amount of any one epitope exposed to the solution varies somewhat from protein to protein, the amount of bound epitope was not found to be limiting within the useful range of the ELISA.

ELISA Tests:

The standard procedure for the ELISA tests was as follows: human serum samples were diluted 1:100 in specimen diluent (10% fetal bovine serum in PBS pH 9.0) and 100 µl of each sample added to ELISA plate microwells that had been coated with antigen as described above. Following incubation for 1 hour at 37°C, the samples were removed and the plates washed three times in TBS-Tween™ (0.5 M Tris pH 7.2; 1.5 M NaCl; 0.5% Tween™). Goat anti-human antisera conjugated to alkaline phosphatase specific for either IgM (Fc) or IgG (Fab), (Jackson Immuno Research Laboratories) was diluted 1:1000 in PBS, pH 7.4 and 100 µl of the solution added to each well. Following incubation for thirty minutes at 37°C, the plates were washed three times with TBS-Tween™ and 100 µl of substrate solution (5 mg of p-nitrophenylphosphate tablets dissolved in 1X diethanolamine substrate buffer to yield a 2 mg/ml solution - Kirkegaard Perry Laboratory) was added to each well. The plates were incubated for thirty minutes at 37°C and 100 µl of stop solution (5 % EDTA) was added to each well. The absorbance at 410 nm was read on a microplate reader (Dynatech). A sample was considered positive if it produced an average absorbance greater than the mean of the negative controls plus three standard deviations. Cross-reactivity was measured against serum from patients with syphilis, systemic lupus erythematosus, rheumatoid arthritis as well as endemic field workers and non-endemic field worker.

Using the above-described ELISA test, serum from various patients was tested. Patients with Erythema Migrans Acute (EMA) had early, localized infections, typified

by the presence of well-defined erythemamigvans (EM) in patients from an endemic area. Patients with Early Disseminated (EA), are Acute Disseminated (AcD) infections were typified by EM and one of the following: additional EM lesions, AV block, neurological abnormalities (e.g., seventh nerve palsy), or meningitis. Patients with

5 Acute Convalescent (AcC) were obtained from the same patients as EA and AcD, 2-4 weeks later. Serum was also tested from the CDC from patients with well documented Syphilis (S), serum was also obtained from SUNY at Stony Brook, Division of Rheumatology from patients with well documented systemic Lupus Erythematosus (SLE) or patients with well documented Rheumatoid Arthritis (RA). Endemic field

10 worker sera (End), were obtained from outdoor workers from Long Island, which is endemic for Lyme disease. Non-endemic sera (Nedn) were obtained from outdoor workers from Arizona, which is not endemic for Lyme disease. In addition, serum was tested from endemic field workers (End) and non-endemic field workers (NEnd). Polypeptides of the present invention were used to test these various sera as summarized

15 in Figure 8.

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Table V

Polypeptide	SEQ ID NO.:* (DNA)	SEQ ID NO: (POLYPEPTIDE)
C1 unlipidated	5	6
C2 unlipidated	7	8
¹ C1	9	10
C2	11	12
C5	13	14
C7	15	16
C10	17	18
C11	19	20
C12	21	22
C1C10 ²	23	24
C1C12	25	26
B31C10 ³	27	28
B31C12	29	30
C2C7	31	32
C2C10	33	34
C2C12	35	36
C5C7	37	38
C5C10	39	40
C5C12	41	42

¹ C1-C12 are *OspC* genes/proteins with lipidation signal.

² C2C10 and other compound C names refer to chimeric *OspC* proteins wherein the N-terminal portion of the chimera is derived from a first *ospC* allele and the C-

terminal portion of the chimeric molecule is derived from second *ospC* allele, as described herein. The polypeptides were not lipidated.

EXAMPLE 4: MICE IMMUNIZATION WITH OSPC CHIMERIC PROTEINS AS

5 IMMUNOGEN

Female BALB/c mice, four-five weeks old, were immunized with 5 µg of OspC chimeric proteins in 100 µl of aluminum hydroxide adjuvant by SC (subcutaneous) injection. Five mice were used for each group. For the negative control, five female BALB/c mice were immunized with 100 µl of aluminum hydroxide adjuvant only.

- 10 Two weeks after immunization, the mice received a boost with the same antigen and two weeks after that an equal boost was administered. One week after each boost, blood was drawn from each mouse (including negative controls) and the serum was tested, using the ELISA method described above, for the presence of the respective anti-OspC chimeric protein antibodies.

- 15 Mice were immunized with chimeric proteins as follows in Table VI.

TABLE VI

	Immunogen	SEQIDNO.:(polypeptide)	OspC Family
	LipCB31 ¹	44 (DNA 43)	A
	LipC12 ²	22 (DNA 21)	K
5	UnlipC2 ³	8	B
	UnlipC2C7 ⁴	32	B/E
	UnlipC2C10	34	B/I
	UnlipC2C12	36	B/K
	UnlipC5C10	40	E/I
10	UnlipC5C12	42	E/K

¹ “Lip” means lipidated N-terminus, Lip CB31 is OspC protein from *B. burgdorferi* strain B31.
² The number immediately after “C” refers to the particular allele of OspC as described herein.
³ “Unlip” means the unlipidated form of the N-terminus.

Several types of single OspCs from *B. burgdorferi sensu stricto*, OspCB31, OspC2, OspC5, OspC7, OspC10, OspC12 and a single OspC from *B. afzelii*, Ctro, were used as the antigens in an ELISA to test the serum collected from the immunized mice. As shown in Figures 2 and 3, unlipC2C10 and unlipC2C12 elicited an immune

20 response in the form of antibodies, (a humoral response) against a broad range of *ospC* families, after the first and second bleeds, respectively. The serum from unlipC2C10, unlipC2C12, LipCB31 and LipC12 immunized mice was then used to test against single OspC polypeptides from several strains of the three major *Borrelia* gene species *Borrelia burgdorferi*, *Borrelia afzelii* and *Borrelia garinii*.

25 As shown in Figure 4, 13 different strains of *B. burgdorferi sensu stricto* (*B.b.s.s.*) were tested for reactivity with the above described sera. Sera from mice immunized with both LipCB31 and LipC12, which were the gold standard of this

experiment, detected 12/13 of the *B.b.s.s.* strains tested. Sera from mice immunized with unlipidated C2C12 detected 8/13 of the strains tested. Use of unlipidated forms of these proteins as vaccine immunogens or diagnostic antigens is desirable because the product yield by the expression vector is much greater and the proteins are much easier to purify. These two reasons alone made the production of these proteins less expensive.

As shown in Figure 5, chimeric proteins unlipC2C10 and unlipC2C12 of the present invention elicited an immune response that detected 5/6, and 6/6 of the strains tested, as compared to the gold standard lipidated proteins LipC12 and LipCB31, which detected 5/6 and 3/6 of the strains, respectively. When compared to the parental unlipidated OspC2 (rOspC2), the chimeric proteins unlipC2C10 and unlipC2C12 elicited an immune response and detected more strains than the gold standard ((0/6) versus (5/6) and (6/6) respectively). This result was unforeseen and unexpected.

In another experiment, as shown in Figures 6 and 7, chimeric proteins of the present invention elicited a significant immune response across all the 18 different strains of *B. afzelii* (Fig. 6) and all the 21 different strains of *B. garinii* (Fig. 7). For example, the chimeras unlipC2C10 and unlipC2C12 detected 12 and 18 of the 18 strains of *B. afzelii*, respectively, as compared to 0/18 detected by the parental unlipidated C2. The same chimeras detected 14 and 20 of the 21 strains of *B. garinii*, respectively, as compared to 0/21 detected by the parental unlipidated C2.

Furthermore, the gold standards LipCB31 and LipC12 detected 2 and 17 of the 18 strains of *B. afzelii*, respectively, and 2 and 15 of the 21 strains of *B. garinii*. These results indicate that, unlike the LipOspCB31, LipOspC12 and unlipOspC2, the unlipidated C2C10 and unlipidated C2C12 used as immunogens elicited a significant immune response across all the different strains of *B. burgdorferi*, *B. afzelii* and *B. garinii* tested.

Additional chimeras were constructed and are listed in Table VII.

TABLE VII

OspC Polypeptides and Chimeric Polypeptides of the Present Invention

	POLYPEPTIDE	SEQ ID NO.:(DNA)	(POLYPEPTIDES)
	¹ unlip OspC kkp(55-621*)	45	46
5	unlip OspC PKO	47	48
	unlip OspC TRO	49	50
	² unlip OspC-55B31/ 58PKO/56TRO	51	52
	unlip OspC1-TRO	53	54
10	unlip OspC-TRO	55	56
	³ Blip OspC1C10	59	60
	BlipOspC12	61	62
	Blip OspC1-TR0	77	78
	Blip OspC2C7	67	78
15	Blip OspC2C10	63	64
	Blip OspC2C12	65	66
	Blip OspC2-TRO	69	70
	Blip OspC5C7	75	76
	Blip OspC5C10	71	72
20	Blip OspC5C12	73	74
	Blip OspCB31C10	79	80
	Blip OspCB31C12	81	82
	Blip OspCPkoTro	83	84
25	Blip OspC- 55B31/58Pko/56Tro	85	86

¹Ulip means the polypeptide is unlipidated.²An OspC chimera comprised of 3 OspC polypeptides.

³Blip means the polypeptide is lipidated due to the gene having the OspB lipidation signal on the 5' terminus.

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that
5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims.

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CLAIMS

What is claimed is:

1. A composition comprising OspC polypeptides from Lyme Disease causing *Borrelia* wherein either:
 - 5 a) said composition comprises one or more OspC polypeptides or immunogenic fragments thereof from at least two *Borrelia burgdorferi* OspC families selected from the group consisting of: A, B, I and K, excepting the combination consisting of two OspC proteins wherein one OspC protein is from family A and the second OspC protein is from
10 family I, or;
 - b) said composition comprises at least one OspC polypeptide or immunogenic fragment thereof from each of *Borrelia afzelii* OspC families A and B.
2. The composition of Claim 1 comprising one or more OspC polypeptides or
15 fragments thereof from each of *Borrelia burgdorferi* families of the group of subpart a).
3. The composition of Claim 1, wherein said OspC polypeptide or fragment thereof comprises the OspC protein variable region.
4. The composition of Claim 3, wherein said OspC polypeptide or fragment
20 thereof is encoded by a nucleic acid comprising nucleotide 26 to about nucleotide 621 of an *ospC* gene.

5. The composition of Claim 3, wherein said OspC polypeptide or fragment thereof is encoded by a nucleic acid comprising nucleotide 53 to about nucleotide 570 of an *ospC* gene.
6. The composition of Claim 1, wherein at least two of said OspC polypeptides or immunogenic fragments thereof are fused together in a single protein, encoded by a single nucleic acid, wherein polypeptides in said fusion protein are not found in the same configuration in a naturally occurring OspC protein.
7. The composition of Claim 1, wherein the *ospC* genes encoding the OspC polypeptides within a given OspC family are at least 98% identical at the nucleic acid level.
8. The composition of Claim 7, wherein *Borrelia burgdorferi* OspC family A comprises strains B31, CA4, HII, IPI, IP2, IP3, L5, PIF, Pka, Txgw and strains containing *ospC* allele OC1.
9. The composition of Claim 7, wherein *Borrelia burgdorferi* OspC family B comprises strains 35B808, 61 BV3, BUR, DK7, PB3, Z57 and strains containing *ospC* genes OC2 and OC3.
10. The composition of Claim 7, wherein *Borrelia burgdorferi* OspC family I comprises strains 297, HB19 and strains containing *ospC* gene OC10, wherein strain 297 is characterized by *ospC* of GenBank accession number L42893.
11. The composition of Claim 7, wherein *Borrelia burgdorferi* OspC family K comprises strains 272, 297, 28354, KIPP, MUL and strains containing *ospC*

gene OC12 and OC13, wherein strain 297 is characterized by *ospC* of GenBank accession number U08284.

12. The composition of Claim 1, wherein *Borrelia afzelii* OspC family A comprises strains Pbo, Pwud, PKO, Pgau, DK2, DK3, DK21, DK8, Bfox and JSB.
- 5 13. The composition of Claim 1, wherein *Borrelia afzelii* OspC family B comprises strains DK5, ACA1, DK9, XB18h, Ple and 134M.
14. A method of immunizing an animal against Lyme disease, comprising administering a composition comprising at least two OspC polypeptides from Lyme Disease causing *Borrelia* wherein either:
- 10 a) said composition comprises one or more OspC polypeptides or fragments thereof from at least two *Borrelia burgdorferi* OspC families selected from the group consisting of: A, B, I and K, excepting the combination consisting of two OspC proteins wherein one OspC protein is from OspC family A and the second OspC protein is from OspC
- 15 family I, or;
- b) said composition comprises at least one OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families A and B.
15. The method of Claim 14, wherein the composition comprises one or more OspC polypeptides or fragments thereof from each of *Borrelia burgdorferi* families of
- 20 the group of subpart a).
16. The method of Claim 14, wherein said OspC polypeptide or fragment thereof comprises the OspC protein variable region.

17. The method of Claim 14, wherein said OspC polypeptide or fragment thereof is encoded by a nucleic acid comprising nucleotide 26 to about nucleotide 621 of an *ospC* gene.
18. The method of Claim 14, wherein said OspC polypeptide or fragment thereof is encoded by a nucleic acid comprising nucleotide 53 to about nucleotide 570 of an *ospC* gene.
19. The method of Claim 14, wherein at least two of said OspC polypeptides or immunogenic fragments thereof are fused together in a single protein, encoded by a single nucleic acid, wherein polypeptides in said fusion protein are not found in the same configuration in a naturally occurring OspC protein.
20. The method of Claim 14, wherein the *ospC* gene encoded the OspC polypeptides within a given OspC family are at least 98% identical at the nucleic acid level.
21. The method of Claim 14, wherein *Borrelia burgdorferi* OspC family A comprises strains B31, CA4, HII, IPI, IP2, IP3, L5, PIF, Pka, Txgw and strains containing *ospC* allele OC1.
22. The method of Claim 14, wherein *Borrelia burgdorferi* OspC family B comprises strains 35B808, 61 BV3, BUR, DK7, PB3, Z57 and strains containing *ospC* genes OC2 and OC3.

23. The method of Claim 14, wherein *Borrelia burgdorferi* OspC family I comprises strains 297, HB19 and strains containing *ospC* gene OC10, wherein strain 297 is characterized by *ospC* of GenBank accession number L42893.
24. The method of Claim 14, wherein *Borrelia burgdorferi* OspC family K comprises strains 272, 297, 28354, KIPP, MUL and strains containing *ospC* gene OC12 and OC13, wherein strain 297 is characterized by *ospC* of GenBank accession number U08284.
25. The method of Claim 14, wherein *Borrelia afzelii* OspC family A comprises strains Pbo, Pwud, PKO, Pgau, DK2, DK3, DK21, DK8, Bfox and JSB.
26. The method of Claim 14, wherein *Borrelia afzelii* OspC family B comprises strains DK5, ACA1, DK9, XB18h, Ple and 134M.
27. A method of detecting an immune response to Lyme Disease causing *Borrelia* in a host sample, comprising;
- a) contacting the host sample with a composition comprising OspC polypeptides from Lyme disease causing strains of *Borrelia*, such that anti-OspC antibodies, if present in said sample bind to said OspC polypeptides; wherein
- i) said composition comprises one or more OspC polypeptides or fragments thereof from at least two *Borrelia burgdorferi* OspC families selected from the group consisting of: A, B, I and K, excepting the combination consisting of two OspC proteins wherein one OspC protein is from family A and the second OspC protein is from family I, or;

-50-

- ii) said composition comprises at least one OspC polypeptide or fragment thereof from each of *Borrelia afzelii* OspC families A and B; and
- b) detecting antibodies that have bound said OspC peptides; thereby
5 detecting an immune response to Lyme disease causing *Borrelia*.
28. The method of Claim 27, wherein said OspC polypeptide or fragment thereof comprises the OspC protein variable region.
29. The composition of Claim 27, wherein said OspC polypeptide or fragment thereof is encoded by a nucleic acid comprising nucleotide 26 to about
10 nucleotide 621 of an *ospC* gene.
30. The composition of Claim 27, wherein said OspC polypeptide or fragment thereof is encoded by a nucleic acid comprising nucleotide 53 to about nucleotide 570 of an *ospC* gene.
31. The composition of Claim 27, wherein at least two of said OspC polypeptides
15 or immunogenic fragments thereof are fused together in a single protein, encoded by a single nucleic acid, wherein polypeptides in said fusion protein are not found in the same configuration in a naturally occurring OspC protein.
32. The method of Claim 27, wherein the *ospC* genes encoding the OspC polypeptides within a given OspC family are at least 98% identical at the
20 nucleic acid level.

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33. The method of Claim 32, wherein *Borrelia burgdorferi* OspC family A comprises strains B31, CA4, HIL, IPI, IP2, IP3, L5, PIF, Pka, Txgw and strains containing *ospC* allele OC1.
34. The method of Claim 32, wherein *Borrelia burgdorferi* OspC family B comprises strains 35B808, 61 BV3, BUR, DK7, PB3, Z57 and strains containing *ospC* genes OC2 and OC3.
35. The method of Claim 32, wherein *Borrelia burgdorferi* OspC family I comprises strains 297, HB19 and strains containing *ospC* gene OC10, wherein strain 297 is characterized by *ospC* of GenBank accession number L42893.
36. The method of Claim 32, wherein *Borrelia burgdorferi* OspC family K comprises strains 272, 297, 28354, KIPP, MUL and strains containing *ospC* gene OC12 and OC13, wherein strain 297 is characterized by *ospC* of GenBank accession number U08284.
37. The method of Claim 32, wherein *Borrelia afzelii* OspC family A comprises strains Pbo, Pwud, PKO, Pgau, DK2, DK3, DK21, DK8, Bfox and JSB.
38. The method of Claim 32, wherein *Borrelia afzelii* OspC family B comprises strains DK5, ACA1, DK9, XB18h, Ple and 134M.
39. A chimeric protein comprising OspC polypeptides from two or more Lyme Disease causing OspC families of Lyme Disease causing *Borrelia* wherein said chimeric protein comprises:

- 5 a) a first OspC polypeptide encoded by a nucleic acid comprising a
sequence from about nucleotide 26 to about nucleotide 621 of an *ospC*
gene from a first OspC family and
b) a second OspC polypeptide encoded by a nucleic acid comprising a
sequence from about nucleotide 28 to about nucleotide 570 of an *ospC*
gene from a second OspC family.
40. The chimeric protein of Claim 39, wherein said OspC families are selected from
the group consisting of: *Borrelia burgdorferi* OspC families A, B, I and K, and
Borrelia afzelii OspC families A and B.
- 10 41. A chimeric protein comprising OspC polypeptides from two or more Lyme
Disease causing OspC families of Lyme Disease causing *Borrelia* wherein said
chimeric protein comprises:
15 a) a first OspC polypeptide encoded by a nucleic acid comprising a
sequence from about nucleotide 53 to about nucleotide 570 of an *ospC*
gene from a first OspC family and
b) a second OspC polypeptide encoded by a nucleic acid comprising a
sequence from about nucleotide 28 to about nucleotide 570 of an *ospC*
gene from a second OspC family.
42. The chimeric protein of Claim 41, wherein said protein is unlipidated.
- 20 43. A chimeric OspC protein selected from the group consisting of: SEQ Id Nos:
24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72,
74, 76, 78, 80, 82, 84 and 86.

44. An isolated nucleic acid encoding a chimeric protein wherein said protein comprises OspC polypeptides from two or more Lyme Disease causing OspC families of Lyme Disease causing *Borrelia* wherein said chimeric protein comprises:
- 5 a) a first OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 26 to about nucleotide 621 of an *ospC* gene from a first OspC family and
- b) a second OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 28 to about nucleotide 570 of an *ospC* gene from a second OspC family.
- 10
45. The nucleic acid of Claim 44, wherein said OspC families are selected from the group consisting of: *Borrelia burgdorferi* OspC families A, B, I and K, and *Borrelia afzelii* OspC families A and B.
46. The nucleic acid of Claim 44, wherein said protein is unlipidated.
- 15 47. A isolated nucleic acid comprising OspC polypeptides from two or more Lyme Disease causing OspC families of Lyme Disease causing *Borrelia* wherein said isolated nucleic acid comprises:
- a) a first OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 53 to about nucleotide 570 of an *ospC* gene from a first OspC family and
- 20 b) a second OspC polypeptide encoded by a nucleic acid comprising a sequence from about nucleotide 28 to about nucleotide 570 of an *ospC* gene from a second OspC family.

48. An isolated nucleic acid selected from the group consisting of : SEQ ID Nos:
23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 51, 53, 55, 56, 59, 61, 63, 65, 67, 69, 71,
73, 75, 77, 79, 81, 83 and 85.

20250324 15:53:00

GROUPS OF *BORRELIA BURGDORFERI* AND *BORRELIA AFZELII*
THAT CAUSE LYME DISEASE IN HUMANS

ABSTRACT OF THE DISCLOSURE

The present invention is drawn to an immunogenic composition comprising

5 OspC polypeptides from Lyme Disease causing *Borrelia*. In one embodiment, the immunogenic composition of the present invention comprises at least one OspC polypeptide or immunogenic fragment thereof from each of *Borrelia burgdorferi* OspC families A, B, I and K. In another embodiment, the immunogenic composition of the present invention comprises at least one OspC polypeptide or immunogenic fragment

10 thereof from each of *Borrelia afzelii* OspC families A and B.

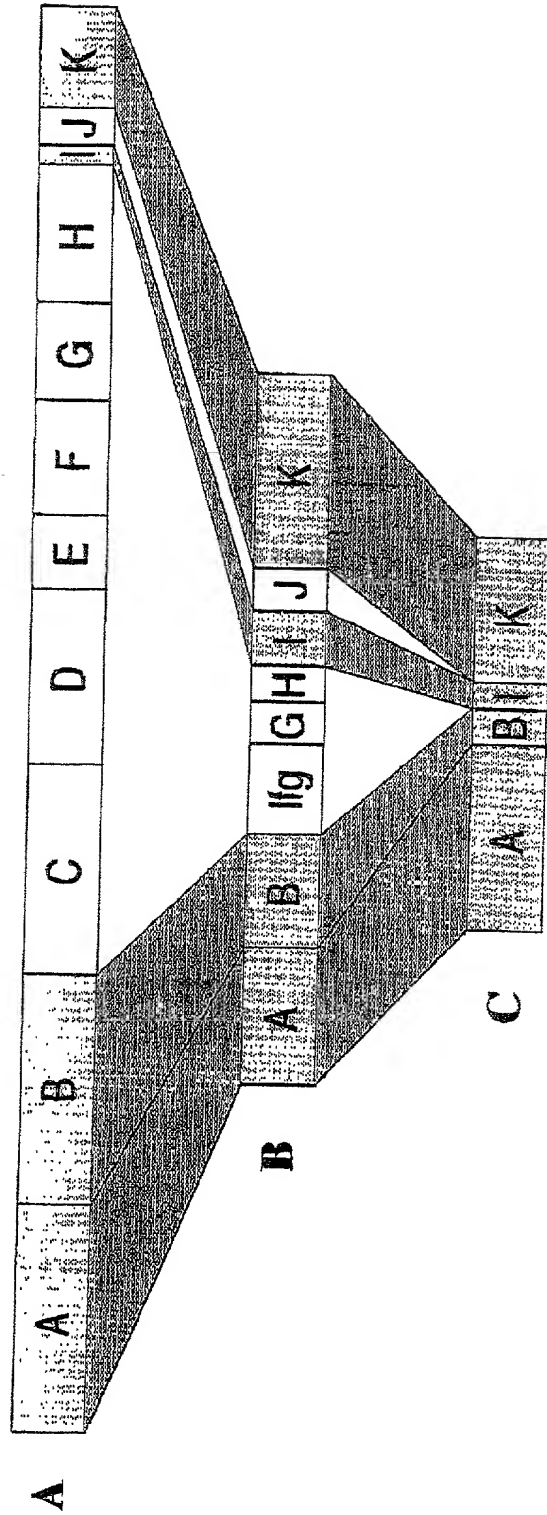


Fig. 1

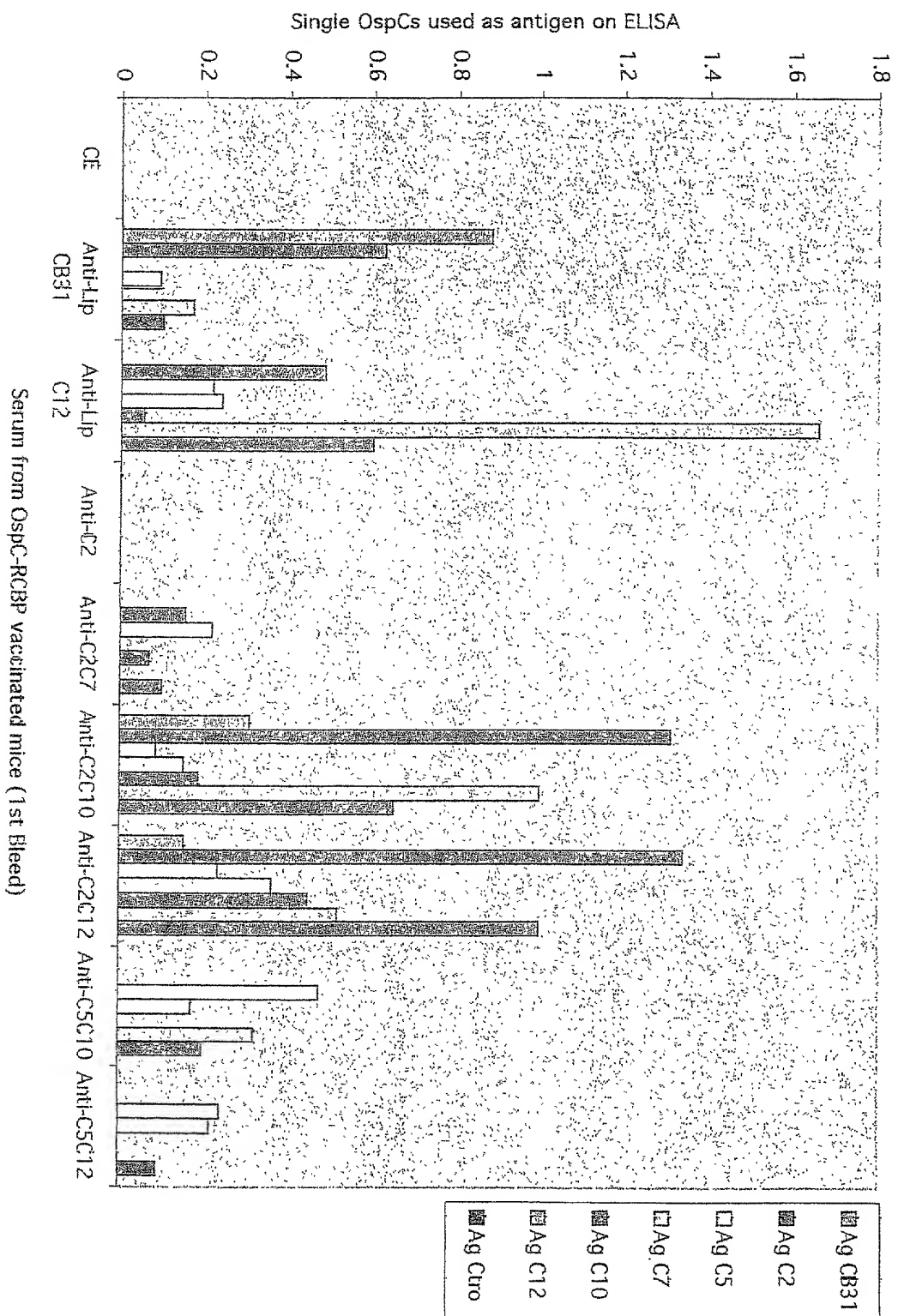


Fig. 2

09596746-061900

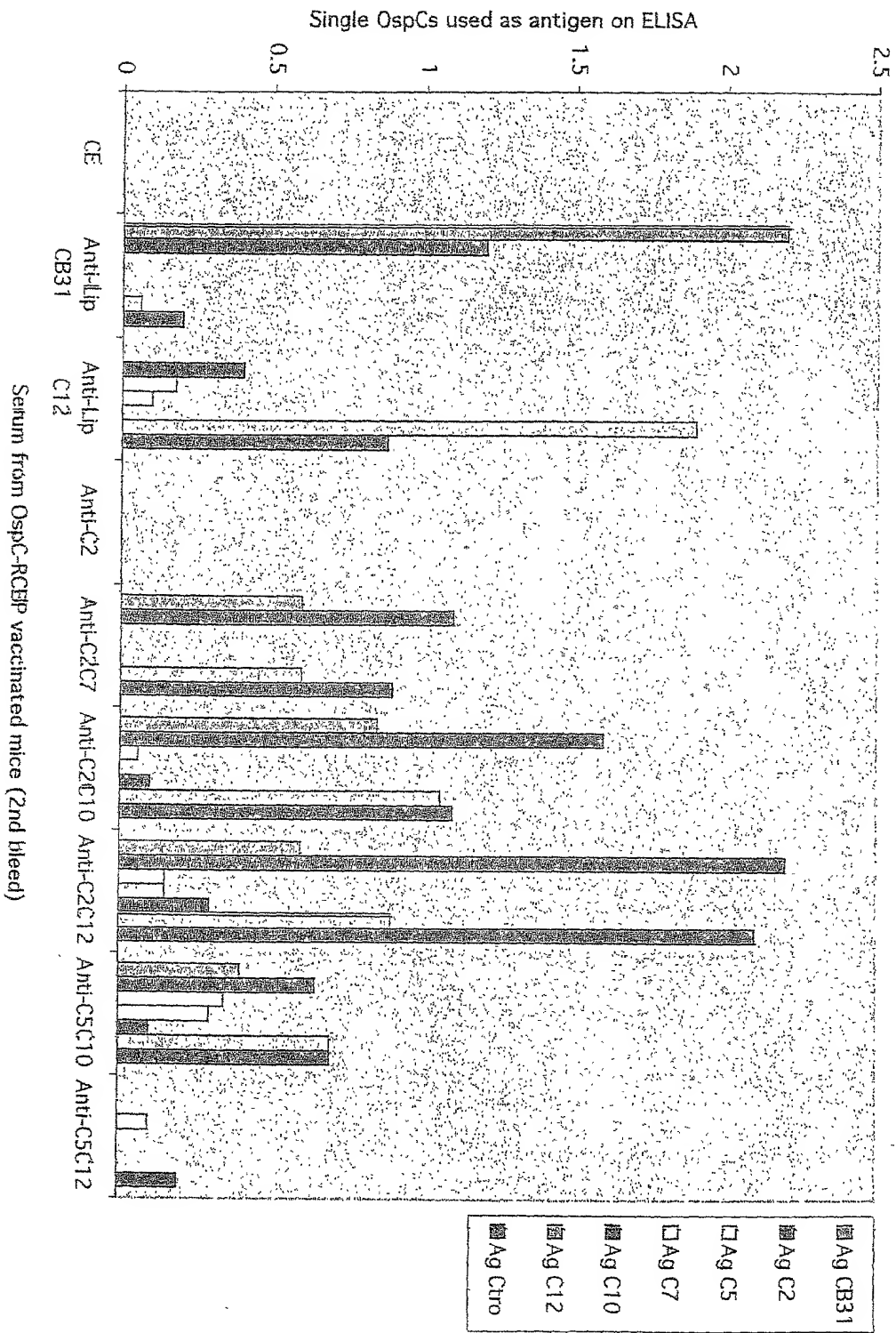


Fig. 3

09595746.061900

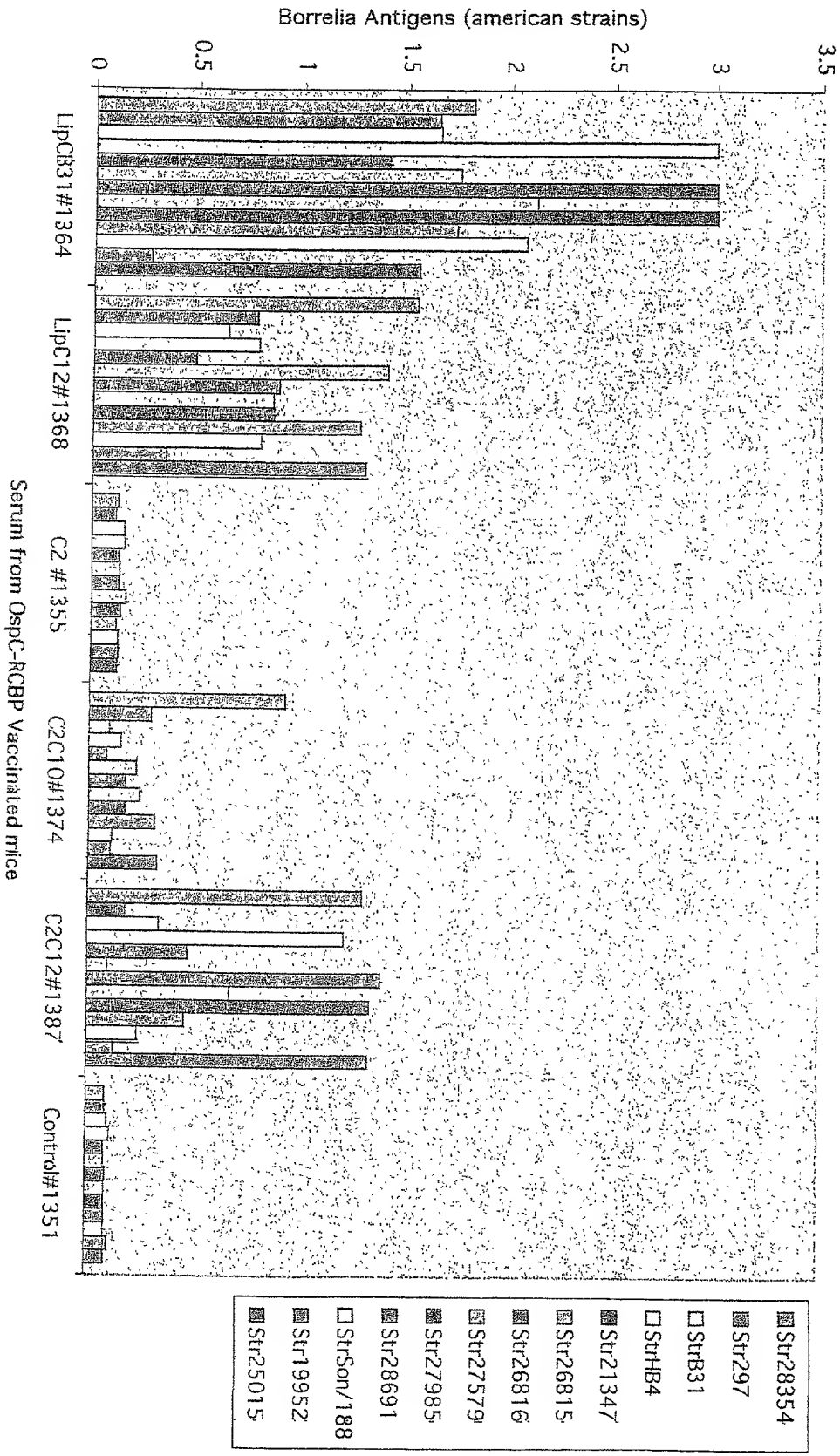


Fig. 4

090906746 . 05.1900

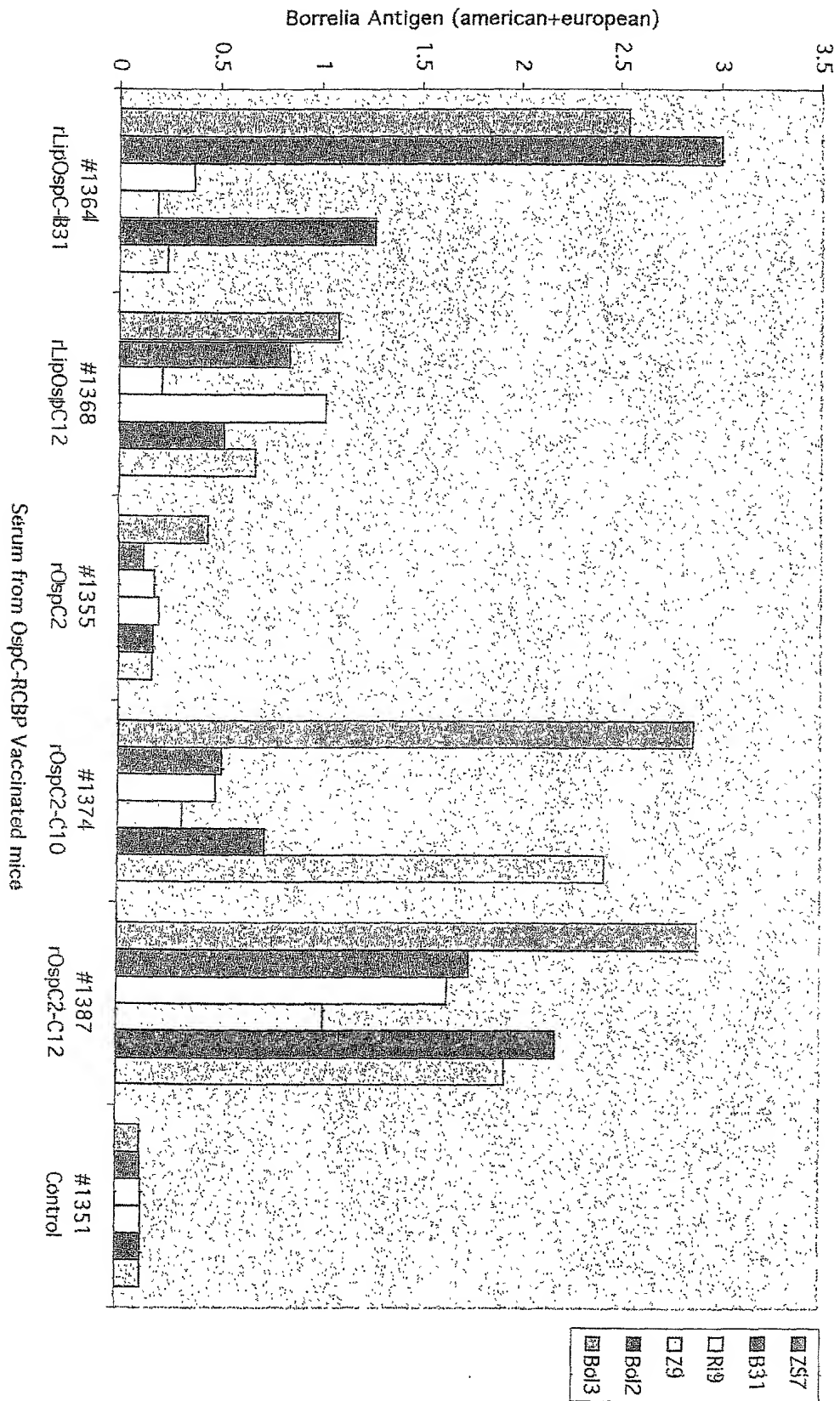


Fig. 5

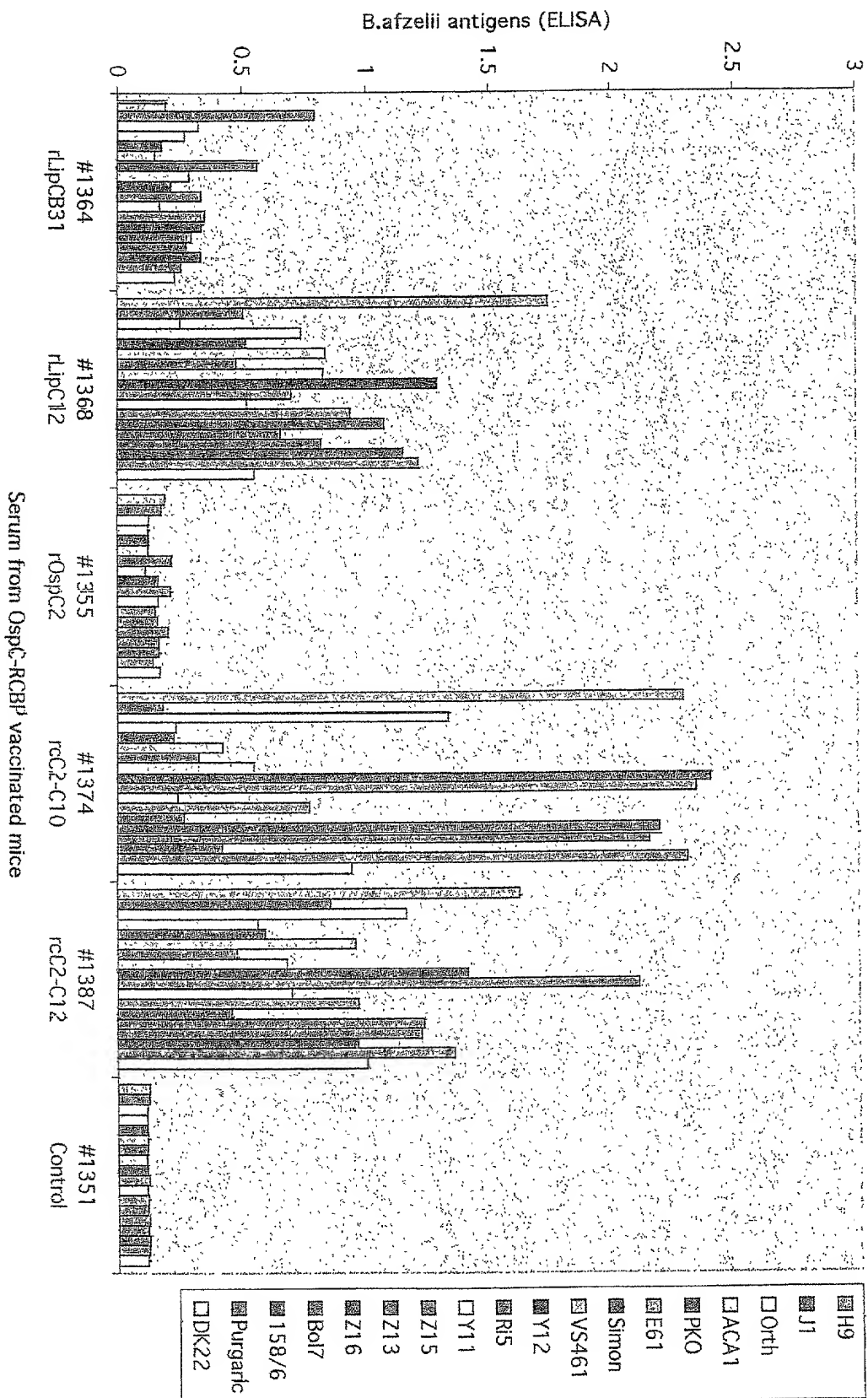


Fig. 6

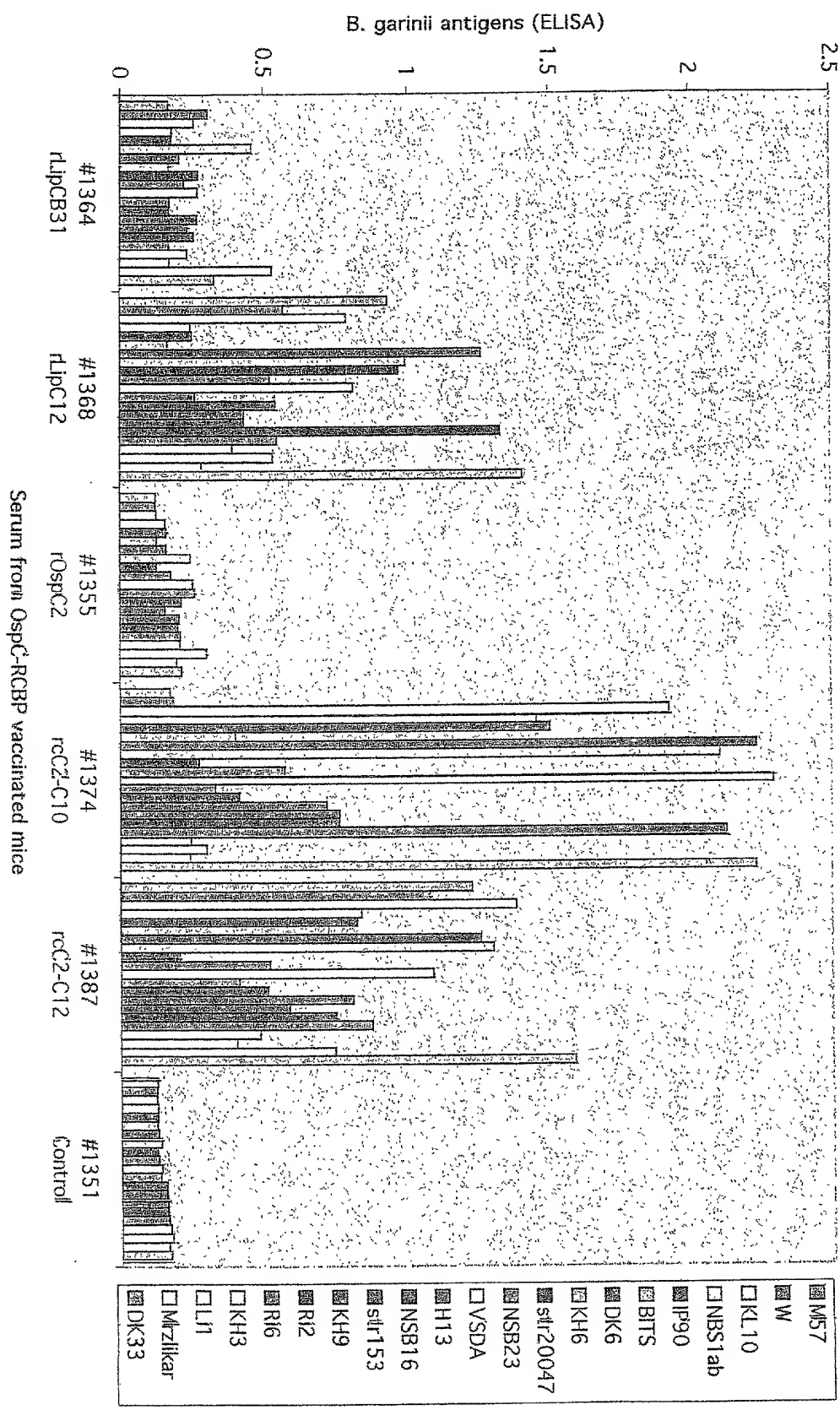


Fig. 7

090916 061900

Early Lyme: #P(total)				Sensitivity		Potential cross-reactivity: #P(Total Tested)				Specificity		
EMA	EA	Ac. Dissem.	Ac. Conval.	#P(Total)	(%)	Syphilis	SLE & RA	Normals End.	Normals NonEnd.	#P(Total)	(%)	
C1 (chrt1)	6(10)	ND	4(10)	8(8)	18(28)	64%	1(10)	1(10)	2(10)	0(8)	4(38)	11%
C2 (chrt2)	4(10)	ND	5(10)	8(8)	17(28)	61%	0(10)	2(10)	2(10)	0(8)	4(38)	11%
C1C10 (chrt3)	7(10)	ND	4(10)	5(8)	16(28)	57%	4(10)	1(10)	2(10)	0(8)	7(38)	18%
C1C12 (chrt4)	2(10)	ND	3(10)	5(8)	10(28)	36%	2(10)	0(10)	0(10)	ND	2(30)	7%
B31C10 (chrt5)	8(10)	ND	6(10)	5(8)	19(28)	68%	2(10)	2(10)	4(10)	0(8)	8(38)	21%
B31C12 (chrt6)	7(10)	ND	6(10)	6(8)	19(28)	68%	1(10)	1(10)	1(10)	0(8)	3(38)	8%
C2C7 (chrt7)	5(10)	6(8)	3(10)	4(7)	18(35)	51%	1(11)	0(10)	1(20)	0(8)	2(49)	4%
C2C10 (chrt8)	4(10)	7(8)	5(10)	4(7)	20(35)	57%	0(11)	0(10)	1(20)	0(8)	1(49)	2%
C2C12 (chrt9)	5(10)	7(8)	6(10)	4(7)	22(35)	63%	0(11)	1(10)	3(20)	0(8)	4(49)	8%
C5C7 (chrt10)	7(10)	ND	4(10)	5(8)	16(28)	57%	2(10)	2(10)	0(10)	ND	4(30)	13%
C5C10 (chrt11)	6(10)	ND	4(10)	5(8)	15(28)	54%	0(10)	0(10)	0(10)	ND	0(30)	0%
C5C12 (chrt12)	8(10)	ND	8(10)	6(8)	22(28)	79%	5(10)	3(10)	3(10)	0(8)	11(38)	29%

EMA = Erythema Migrans Acute
 EA = Acute Disseminated
 Ac. Dissem. = Acute Disseminated
 Ac. Conval. = Acute Convalescent
 #P = Number of positives
 SLE = Systemic Lupus Erythematosus
 RA = Rheumatoid Arthritis
 End. = Endemic Field Workers
 NonEnd. = Non Endemic

Fig. 8

<110> Dattwyler, Raymond J.
Seinost, Gerald
Dykhuizen, Danial
Luft, Benjamin J.
Maria J.C. Gomes-Solecki

<120> Groups of *Borrelia burgdorferi* and
Borrelia afzelii That Cause Lyme Disease in Humans

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35 40 45

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65 70 75 80

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Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336
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100 105 110

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115 120 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
130 135 140

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145 150 155 160

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165 170 175

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 Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
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 35 40 45
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 50 55 60
 Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu
 65 70 75 80
 Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys
 85 90 95
 Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys Lys
 100 105 110
 Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu
 115 120 125
 Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys
 130 135 140
 Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu
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Thr	Glu	Ser 35	Asn	Ala	Val	Val	Leu 40	Ala	Val	Lys	Glu	Val 45	Glu	Thr	Leu
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Gly 65	Asn	Asn	Gly	Leu	Glu 70	Ala	Asn	Gln	Ser	Lys 75	Asn	Thr	Ser	Leu 80	Leu
Ser	Gly	Ala	Tyr	Ala 85	Ile	Ser	Asp	Leu	Ile 90	Ala	Glu	Lys	Leu 95	Asn	Val

Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys
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 Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly
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 85 90 95

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 aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat aaa tta 384
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000745-06100

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Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys Ala
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gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc cct gtt 576
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Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn
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Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu
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Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala
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Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu
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Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala
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Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu	
20 25 30	
aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta ctt gct	144
Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala	
35 40 45	
gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt gct aaa	192
Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys	
50 55 60	
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65 70 75 80	
aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca acc tta	288
Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu	
85 90 95	
ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta aag gaa	336
Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu	
100 105 110	
aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act aaa cta	384
Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu	
115 120 125	
aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat gaa aat	432
Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu Asn	
130 135 140	
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Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly	
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Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys	
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          35          40          45
Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala
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Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn
65          70          75          80
Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile
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Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys
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145          150          155          160
Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala
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          50          55          60

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65          70          75          80

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 100 105 110

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 115 120 125

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 130 135 140

caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt gct gca 480
 Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala
 145 150 155 160

gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct 528
 Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala
 165 170 175

caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg 576
 Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
 180 185 190

<210> 14
 <211> 191
 <212> PRT
 <213> Borrelia burgdorferi

<400> 14

Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn
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 Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr
 20 25 30
 Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val
 35 40 45
 Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys
 50 55 60
 Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser
 65 70 75 80
 Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile
 85 90 95
 Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile
 100 105 110
 Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser
 115 120 125
 Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln
 130 135 140
 Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu
 145 150 155 160
 Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln
 165 170 175

atg Met 1	act Thr	tta Leu	ttt Phe	tta Leu 5	ttt Phe	ata Ile	tct Ser	tgt Cys	aat Asn 10	aat Asn	tca Ser	aga Arg	aaa Lys	gat Asp 15	ggg Gly	48
aat Asn	gca Ala	tct Ser	aca Thr 20	aat Asn	tct Ser	gcc Ala	gat Asp	gag Glu 25	tct Ser	gtt Val	aaa Lys	ggg Gly	cct Pro 30	aat Asn	ctt Leu	96
aca Thr	gaa Glu	ata Ile 35	agt Ser	aaa Lys	aaa Lys	att Ile	aca Thr 40	gaa Glu	tct Ser	aac Asn	gca Ala	gtt Val 45	gtt Val	ctg Leu	gcc Ala	144
gtg Val	aaa Lys 50	gaa Glu	gtt Val	gag Glu	acc Thr	tta Leu 55	ctt Leu	gca Ala	tct Ser	ata Ile	gat Asp 60	gaa Glu	ctt Leu	gct Ala	acc Thr	192
aaa Lys 65	gct Ala	att Ile	ggg Gly	aag Lys	aaa Lys 70	ata Ile	ggc Gly	aat Asn	aat Asn	ggg Gly 75	tta Leu	gag Glu	gcc Ala	aat Asn	cag Gln 80	240
agt Ser	aaa Lys	aac Asn	aca Thr	tca Ser 85	ttg Leu	tta Leu	tca Ser	gga Gly	gct Ala 90	tat Tyr	gca Ala	ata Ile	tct Ser	gac Asp 95	cta Leu	288
ata Ile	gca Ala	gaa Glu	aaa Lys 100	tta Leu	aat Asn	gta Val	ttg Leu	aaa Lys 105	aat Asn	gaa Glu	gaa Glu	tta Leu	aag Lys 110	gaa Glu	aag Lys	336
att Ile	gat Asp	aca Thr 115	gct Ala	aag Lys	caa Gln	tgt Cys	tct Ser 120	aca Thr	gaa Glu	ttt Phe	act Thr	aat Asn 125	aaa Lys	cta Leu	aaa Lys	384
agt Ser	gaa Glu 130	cat His	gca Ala	gtg Val	ctt Leu	ggg Gly 135	ctg Leu	gac Asp	aat Asn	ctt Leu	act Thr 140	gat Asp	gat Asp	aat Asn	gca Ala	432
caa Gln 145	aga Arg	gct Ala	att Ile	tta Leu 150	aaa Lys 150	aaa Lys	cat His	gca Ala	aat Asn 155	aaa Lys 155	gat Asp	aag Lys	ggg Gly	gct Ala 160	gca Ala 160	480
gaa Glu	ctt Leu	gaa Glu	aag Lys	tta Leu 165	ttt Phe	aaa Lys	gcg Ala	gta Val	gaa Glu 170	aac Asn	tta Leu	tca Ser	aaa Lys 175	gca Ala 175	gct Ala 175	528

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caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg 576
Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
180 185 190

<210> 16
<211> 191
<212> PRT
<213> borrelia burgdorferi

<400> 16
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20 25 30
Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val
35 40 45
Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys
50 55 60
Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser
65 70 75 80
Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile
85 90 95
Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile
100 105 110
Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser
115 120 125
Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln
130 135 140
Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu
145 150 155 160
Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln
165 170 175
Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
180 185 190

<210> 17
<211> 573
<212> DNA
<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(573)

<400> 17
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Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly
1 5 10 15
aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
20 25 30
aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc 144
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
35 40 45

gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa 192
Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys
50 55 60

gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca 240
Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala
65 70 75 80

gat cac aac gga tca tta ata tca gga gca tat tta att tca aac tta 288
Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu
85 90 95

ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca 336
Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala
100 105 110

gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta 384
Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu
115 120 125

aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat 432
Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn
130 135 140

gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc gct 480
Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala
145 150 155 160

gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca 528
Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala
165 170 175

gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc cct 573
Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro
180 185 190

<210> 18
<211> 190
<212> PRT
<213> Borrelia burgdorferi

<400> 18
Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn
1 5 10 15
Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr
20 25 30
Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val
35 40 45
Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala
50 55 60
Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp
65 70 75 80
His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile
85 90 95
Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu
100 105 110


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Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys
      115      120      125
Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala
      130      135      140
Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp
145      150      155      160
Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala
      165      170      175
Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro
      180      185      190

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<210> 19
 <211> 553
 <212> DNA
 <213> *Borrelia burgdorferi*

<220>
 <221> CDS
 <222> (1)...(553)

<400> 19

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atg act tta ttt tta ttt ata tct tgt aat aat tca gga aaa gat ggg 48
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  1          5          10          15

aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
          20          25          30

aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct 144
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
          35          40          45

gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct act 192
Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
          50          55          60

aaa gct att ggt aaa aaa ata gat aac aat gct ggt ttg ggt gct gaa 240
Lys Ala Ile Gly Lys Lys Ile Asp Asn Asn Ala Gly Leu Gly Ala Glu
  65          70          75          80

gtg ggt caa aac gga tca ttg cta gca gga gct tat gca atc tca act 288
Val Gly Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr
          85          90          95

gta ata ata gaa aaa ttg agc aca tta aaa aat gta gaa gaa tta aaa 336
Val Ile Ile Glu Lys Leu Ser Thr Leu Lys Asn Val Glu Glu Leu Lys
          100          105          110

gaa aaa att aca aag gct aag gat tgt tct gaa aaa ttc act aaa aaa 384
Glu Lys Ile Thr Lys Ala Lys Asp Cys Ser Glu Lys Phe Thr Lys Lys
          115          120          125

tta aaa gat agc cgc gca gag ctt ggt aaa aaa gat gcc agt gat gat 432
Leu Lys Asp Ser Arg Ala Glu Leu Gly Lys Lys Asp Ala Ser Asp Asp
  130          135          140

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000190-01495500

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gat gca aaa aaa gct att tta aaa aca aat caa gct aac gat aag ggt 480
Asp Ala Lys Lys Ala Ile Leu Lys Thr Asn Gln Ala Asn Asp Lys Gly
145 150 155 160

gct aaa gaa ctt aaa gag tta ttt gaa gca gta gaa agc ttg tca aaa 528
Ala Lys Glu Leu Lys Glu Leu Phe Glu Ala Val Glu Ser Leu Ser Lys
165 170 175

gcg gct aaa gag atg cta aac aag t 553
Ala Ala Lys Glu Met Leu Asn Lys
180

<210> 20
<211> 183
<212> PRT
<213> *Borrelia burgdorferi*

<400> 20
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Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr
20 25 30
Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val
35 40 45
Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys
50 55 60
Ala Ile Gly Lys Lys Ile Asp Asn Asn Ala Gly Leu Gly Ala Glu Val
65 70 75 80
Gly Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Val
85 90 95
Ile Ile Glu Lys Leu Ser Thr Leu Lys Asn Val Glu Glu Leu Lys Glu
100 105 110
Lys Ile Thr Lys Ala Lys Asp Cys Ser Glu Lys Phe Thr Lys Lys Leu
115 120 125
Lys Asp Ser Arg Ala Glu Leu Gly Lys Lys Asp Ala Ser Asp Asp Asp
130 135 140
Ala Lys Lys Ala Ile Leu Lys Thr Asn Gln Ala Asn Asp Lys Gly Ala
145 150 155 160
Lys Glu Leu Lys Glu Leu Phe Glu Ala Val Glu Ser Leu Ser Lys Ala
165 170 175
Ala Lys Glu Met Leu Asn Lys
180

<210> 21
<211> 582
<212> DNA
<213> *Borrelia burgdorferi*

<220>
<221> CDS
<222> (1)...(582)

<400> 21
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1 5 10 15

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<210> 22
<211> 193
<212> PRT
<213> Borrelia burgdorferi

<400> 22
Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn
 1          5          10
Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr
          20          25          30

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Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val
 35 40 45
 Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys
 50 55 60
 Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala
 65 70 75 80
 Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu
 85 90 95
 Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu
 100 105 110
 Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu
 115 120 125
 Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn
 130 135 140
 Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala
 145 150 155 160
 Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala
 165 170 175
 Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Ile
 180 185 190
 Val

<210> 23
 <211> 1128
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1128)

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 1 5 10 15

 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

 att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45

 ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60

 ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
 65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta	288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu	
85 90 95	
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag	336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	
100 105 110	
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat	384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
115 120 125	
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta	432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130 135 140	
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta	480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145 150 155 160	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct	528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala	
180 185 190	
atg gta aat aat tca ggg aaa gat ggg aat aca tct gca aat tct gct	624
Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala	
195 200 205	
gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att	672
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile	
210 215 220	
aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg	720
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu	
225 230 235 240	
ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata aaa	768
Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys	
245 250 255	
aac gat gtt agt tta gat aat gag gca gat cac aac gga tca tta ata	816
Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile	
260 265 270	
tca gga gca tat tta att tca aac tta ata aca aaa aaa ata agt gca	864
Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala	
275 280 285	
ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct aag aaa	912
Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys	
290 295 300	
tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca gat ctt	960
Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu	
305 310 315 320	

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<210> 24
<211> 374
<212> PRT
<213> Artificial Sequence
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<213> Artificial Sequence

<223> OspC Chimera

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Thr	Asp	Ser 35	Asn	Ala	Val	Leu 40	Leu	Ala	Val	Lys	Glu 45	Val	Glu	Ala	Leu
Leu	Ser 50	Ser	Ile	Asp	Glu	Ile 55	Ala	Ala	Lys	Ala	Ile 60	Gly	Lys	Lys	Ile
His 65	Gln	Asn	Asn	Gly	Leu 70	Asp	Thr	Glu	Tyr	Asn 75	His	Asn	Gly	Ser	Leu 80
Leu	Ala	Gly	Ala	Tyr 85	Ala	Ile	Ser	Thr	Leu 90	Ile	Lys	Gln	Lys	Leu 95	Asp
Gly	Leu	Lys	Asn 100	Glu	Gly	Leu	Lys	Glu 105	Lys	Ile	Asp	Ala	Ala	Lys	Lys
Cys	Ser	Glu 115	Thr	Phe	Thr	Asn	Lys 120	Leu	Lys	Glu	Lys	His 125	Thr	Asp	Leu
Gly	Lys 130	Glu	Gly	Val	Thr	Asp 135	Ala	Asp	Ala	Lys	Glu 140	Ala	Ile	Leu	Lys
Thr 145	Asn	Gly	Thr	Lys	Thr 150	Lys	Gly	Ala	Glu	Glu 155	Leu	Gly	Lys	Leu	Phe 160
Glu	Ser	Val	Glu	Val 165	Leu	Ser	Lys	Ala	Ala 170	Lys	Glu	Met	Leu	Ala 175	Asn
Ser	Val	Lys	Glu 180	Leu	Thr	Ser	Pro	Val 185	Val	Ala	Glu	Ser	Pro 190	Ala	Met
Val	Asn 195	Asn	Ser	Gly	Lys	Asp	Gly 200	Asn	Thr	Ser	Ala	Asn 205	Ser	Ala	Asp
Glu	Ser 210	Val	Lys	Gly	Pro	Asn 215	Leu	Thr	Glu	Ile	Ser 220	Lys	Lys	Ile	Thr
Glu 225	Ser	Asn	Ala	Val	Val 230	Leu	Ala	Val	Lys	Glu 235	Val	Glu	Thr	Leu	Leu 240
Thr	Ser	Ile	Asp	Glu 245	Leu	Ala	Lys	Ala	Ile 250	Gly	Lys	Lys	Ile	Lys 255	Asn

Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser
 260 265 270
 Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile
 275 280 285
 Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys
 290 295 300
 Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly
 305 310 315 320
 Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr
 325 330 335
 Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu
 340 345 350
 Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser
 355 360 365
 Val Lys Glu Leu Thr Ser
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<210> 25
 <211> 1124
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1124)

<400> 25
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 1 5 10 15

 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

 att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45

 ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60

 ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
 65 70 75 80

 ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85 90 95

 gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110

005790-973556

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat	384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
115 120 125	
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta	432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130 135 140	
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta	480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145 150 155 160	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct	528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala	
180 185 190	
atg gta aat aat tca gga aaa gat ggg aat aca tct gca aat tct gct	624
Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala	
195 200 205	
gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att	672
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile	
210 215 220	
aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa act ttg	720
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu	
225 230 235 240	
ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa aaa ata	768
Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile	
245 250 255	
caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga aca ttg	816
Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu	
260 265 270	
tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa tta gat	864
Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp	
275 280 285	
gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat gct aag	912
Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys	
290 295 300	
aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat gcg caa	960
Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln	
305 310 315 320	
ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct att tta	1008
Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu	
325 330 335	
ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa aag cta	1056
Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu	
340 345 350	


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ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg ctt gct 1104
Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala
      355                      360                      365

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aat tca gtt aaa gag ctt ac 1124
Asn Ser Val Lys Glu Leu
      370

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<210> 26
<211> 373
<212> PRT
<213> Artificial Sequence

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<220>
<223> OspC Chimera

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<400> 26
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
 1      5      10
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
      20      25      30
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
      35      40      45
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
      50      55      60
His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser Leu
      65      70      75      80
Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp
      85      90      95
Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys
      100      105      110
Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu
      115      120      125
Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys
      130      135      140
Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe
      145      150      155      160
Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn
      165      170      175
Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala Met
      180      185      190
Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp
      195      200      205
Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr
      210      215      220
Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu
      225      230      235      240
Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln
      245      250      255
Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu
      260      265      270
Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly
      275      280      285
Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys
      290      295      300
Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu
      305      310      315      320

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006746-06100

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<210> 27
<211> 1137
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera
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<400> 27																	
atg	gct	tgt	aat	aat	tca	ggg	aaa	gat	ggg	aat	aca	tct	gca	aat	tct	48	
Met	Ala	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser		
1				5					10					15			
gct	gat	gag	tct	ggt	aaa	ggg	cct	aat	ctt	aca	gaa	ata	aat	aaa	aaa	96	
Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Asn	Lys	Lys		
			20					25					30				
att	acg	gat	tct	aat	gcg	ggt	tta	ctt	gct	gtg	aaa	gag	ggt	gaa	gcg	144	
Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	Ala		
		35					40					45					
ttg	ctg	tca	tct	ata	gat	gaa	att	gct	gct	aaa	gct	att	ggt	aaa	aaa	192	
Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile	Ala	Ala	Lys	Ala	Ile	Gly	Lys	Lys		
	50					55					60						
ata	cac	caa	aat	aat	ggt	ttg	gat	acc	gaa	aat	aat	cac	aat	gga	tca	240	
Ile	His	Gln	Asn	Asn	Gly	Leu	Asp	Thr	Glu	Asn	Asn	His	Asn	Gly	Ser		
65					70					75					80		
ttg	tta	gcg	gga	gct	tat	gca	ata	tca	acc	cta	ata	aaa	caa	aaa	tta	288	
Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu		
				85					90					95			
gat	gga	ttg	aaa	aat	gaa	gga	tta	aag	gaa	aaa	att	gat	gcg	gct	aag	336	
Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu	Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys		
			100					105					110				
aaa	tgt	tct	gaa	aca	ttt	act	aat	aaa	tta	aaa	gaa	aaa	cac	aca	gat	384	
Lys	Cys	Ser	Glu	Thr	Phe	Thr	Asn	Lys	Leu	Lys	Glu	Lys	His	Thr	Asp		
		115					120					125					
ctt	ggt	aaa	gaa	ggt	ggt	act	gat	gct	gat	gca	aaa	gaa	gcc	att	tta	432	
Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu		
	130					135					140						

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
 Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
 145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa 576
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
 180 185 190

aaa cct tcc atg gta aat aat tca ggg aaa gat ggg aat aca tct gca 624
 Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
 195 200 205

aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt 672
 Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
 210 215 220

aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt 720
 Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val
 225 230 235 240

gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa 768
 Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys
 245 250 255

aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga 816
 Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly
 260 265 270

tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa 864
 Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys
 275 280 285

ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag 912
 Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys
 290 295 300

gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac 960
 Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His
 305 310 315 320

aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc 1008
 Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala
 325 330 335

att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa 1056
 Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu
 340 345 350

aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg 1104
 Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met
 355 360 365

ctt act aat tca gtt aaa gag ctt aca agc taa 1137
 Leu Thr Asn Ser Val Lys Glu Leu Thr Ser *
 370 375

<210> 28
 <211> 378
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<400> 28

Met	Ala	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	1	5	10	15
Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Asn	Lys	Lys	20	25	30	
Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	35	40	45	
Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile	Ala	Ala	Lys	Ala	Ile	Gly	Lys	Lys	50	55	60	
Ile	His	Gln	Asn	Asn	Gly	Leu	Asp	Thr	Glu	Asn	Asn	His	Asn	Gly	Ser	65	70	75	80
Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu	85	90	95	
Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu	Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys	100	105	110	
Lys	Cys	Ser	Glu	Thr	Phe	Thr	Asn	Lys	Leu	Lys	Glu	Lys	His	Thr	Asp	115	120	125	
Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu	130	135	140	
Lys	Ala	Asn	Gly	Thr	Lys	Thr	Lys	Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu	145	150	155	160
Phe	Glu	Ser	Val	Glu	Val	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	165	170	175	
Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	180	185	190	
Lys	Pro	Ser	Met	Val	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	195	200	205	
Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	210	215	220	
Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Val	225	230	235	240
Glu	Thr	Leu	Leu	Thr	Ser	Ile	Asp	Glu	Leu	Ala	Lys	Ala	Ile	Gly	Lys	245	250	255	
Lys	Ile	Lys	Asn	Asp	Val	Ser	Leu	Asp	Asn	Glu	Ala	Asp	His	Asn	Gly	260	265	270	
Ser	Leu	Ile	Ser	Gly	Ala	Tyr	Leu	Ile	Ser	Asn	Leu	Ile	Thr	Lys	Lys	275	280	285	
Ile	Ser	Ala	Ile	Lys	Asp	Ser	Gly	Glu	Leu	Lys	Ala	Glu	Ile	Glu	Lys	290	295	300	
Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe	Thr	Ala	Lys	Leu	Lys	Gly	Glu	His	305	310	315	320
Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	Asp	Asn	Ala	Lys	Lys	Ala	325	330	335	
Ile	Leu	Lys	Thr	Asn	Asn	Asp	Lys	Thr	Lys	Gly	Ala	Asp	Glu	Leu	Glu	340	345	350	
Lys	Leu	Phe	Glu	Ser	Val	Lys	Asn	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met	355	360	365	
Leu	Thr	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser							370	375		

006790-04296660

<210> 29
 <211> 1133
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1133)

<400> 29
 atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
 20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
 65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
 Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
 145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175

000190-01435200

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<210> 30
<211> 377
<212> PRT
<213> Artificial Sequence
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<220>

<223> OspC Chimera

<400> 30

Met	Ala	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser
1				5					10					15	
Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Asn	Lys	Lys
			20					25					30		
Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	Ala
		35					40					45			
Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile	Ala	Ala	Lys	Ala	Ile	Gly	Lys	Lys
	50				55						60				
Ile	His	Gln	Asn	Asn	Gly	Leu	Asp	Thr	Glu	Asn	His	Asn	Gly	Ser	
65					70				75					80	
Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu
				85					90					95	
Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu	Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys
			100					105					110		
Lys	Cys	Ser	Glu	Thr	Phe	Thr	Asn	Lys	Leu	Lys	Glu	Lys	His	Thr	Asp
		115					120					125			
Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu
	130					135					140				
Lys	Ala	Asn	Gly	Thr	Lys	Thr	Lys	Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu
145					150				155						160
Phe	Glu	Ser	Val	Glu	Val	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala
				165					170					175	
Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	Val	Val	Ala	Glu	Ser	Pro	Lys
			180					185					190		
Lys	Pro	Ser	Met	Val	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala
		195					200					205			
Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser
		210				215					220				
Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Ile
225				230						235					240
Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	Glu	Leu	Ala	Thr	Lys	Ala	Ile	Gly
				245					250					255	
Lys	Lys	Ile	Gln	Gln	Asn	Gly	Gly	Leu	Ala	Val	Glu	Ala	Gly	His	Asn
			260					265					270		
Gly	Thr	Leu	Leu	Ala	Gly	Ala	Tyr	Thr	Ile	Ser	Lys	Leu	Ile	Thr	Gln
		275					280					285			
Lys	Leu	Asp	Gly	Leu	Lys	Asn	Ser	Glu	Lys	Leu	Lys	Glu	Lys	Ile	Glu
	290					295					300				
Asn	Ala	Lys	Lys	Cys	Ser	Glu	Asp	Phe	Thr	Lys	Lys	Leu	Glu	Gly	Glu
305					310					315					320
His	Ala	Gln	Leu	Gly	Ile	Glu	Asn	Val	Thr	Asp	Glu	Asn	Ala	Lys	Lys
				325					330					335	
Ala	Ile	Leu	Ile	Thr	Asp	Ala	Ala	Lys	Asp	Lys	Gly	Ala	Ala	Glu	Leu
		340						345					350		
Glu	Lys	Leu	Phe	Lys	Ala	Val	Glu	Asn	Leu	Ala	Lys	Ala	Ala	Lys	Glu
		355					360					365			
Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu							
	370					375									

<210> 31

<211> 1112

<212> DNA

<213> Artificial Sequence

<220>

<223> OspC Chimera

<221> CDS

<222> (1)...(1112)

<400> 31

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Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser	
1 5 10 15	
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa	96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg	144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	
ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata	192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile	
50 55 60	
aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg	240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu	
65 70 75 80	
tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt	288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser	
85 90 95	
aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag	336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys	
100 105 110	
aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag	384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln	
115 120 125	
ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta	432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu	
130 135 140	
aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag	480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys	
145 150 155 160	
ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt	528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu	
165 170 175	
gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat	576
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn	
180 185 190	
tca aga aaa gat ggg aat gca tct aca aat tct gcc gat gag tct gtt	624
Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val	
195 200 205	


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aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac 672
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn
210 215 220

gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata 720
Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile
225 230 235 240

gat gaa ctt gct acc aaa gct att ggt aag aaa ata ggc aat aat ggt 768
Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly
245 250 255

tta gag gcc aat cag agt aaa aac aca tca ttg tta tca gga gct tat 816
Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr
260 265 270

gca ata tct gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa 864
Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu
275 280 285

gaa tta aag gaa aag att gat aca gct aag caa tgt tct aca gaa ttt 912
Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe
290 295 300

act aat aaa cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt 960
Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu
305 310 315 320

act gat gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa 1008
Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys
325 330 335

gat aag ggt gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac 1056
Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn
340 345 350

tta tca aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt 1104
Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu
355 360 365

aca agt cc 1112
Thr Ser
370

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<210> 32
<211> 369
<212> PRT
<213> Artificial Sequence

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<220>
<223> OspC Chimera

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<400> 32
Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
1 5 10 15
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
20 25 30

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atg Met 1	gct Ala	tgt Cys	aat Asn	aat Asn 5	tca Ser	ggg Gly	aaa Lys	gat Asp	ggg Gly 10	aat Asn	aca Thr	tct Ser	gca Ala	aat Asn 15	tct Ser	48
gct Ala	gat Asp	gag Glu	tct Ser 20	gtt Val	aaa Lys	ggg Gly	cct Pro	aat Asn 25	ctt Leu	aca Thr	gaa Glu	ata Ile	agt Ser 30	aaa Lys	aaa Lys	96
att Ile	acg Thr	gat Asp 35	tct Ser	aat Asn	gcg Ala	gtt Val 40	tta Leu	ctt Leu	gct Ala	gtg Val	aaa Lys	gag Glu 45	gtt Val	gaa Glu	gcg Ala	144
ttg Leu	ctg Leu 50	tca Ser	tct Ser	ata Ile	gat Asp	gag Glu 55	ctt Leu	gct Ala	aaa Lys	gct Ala	att Ile 60	ggg Gly	aaa Lys	aaa Lys	ata Ile	192
aaa Lys 65	aac Asn	gat Asp	ggg Gly	agt Ser	tta Leu 70	gat Asp	aat Asn	gaa Glu	gca Ala	aat Asn 75	cgc Arg	aac Asn	gag Glu	tca Ser	ttg Leu 80	240
tta Leu	gca Ala	gga Gly	gct Ala	tat Tyr 85	aca Thr	ata Ile	tca Ser	acc Thr	tta Leu 90	ata Ile	aca Thr	caa Gln	aaa Lys	tta Leu 95	agt Ser	288
aaa Lys	tta Leu	aac Asn	gga Gly 100	tca Ser	gaa Glu	ggg Gly	tta Leu 105	aag Lys	gaa Glu	aag Lys	att Ile	gcc Ala	gca Ala 110	gct Ala	aag Lys	336
aaa Lys	tgc Cys	tct Ser 115	gaa Glu	gag Glu	ttt Phe	agt Ser	act Thr	aaa Lys	cta Leu	aaa Lys	gat Asp	aat Asn 125	cat His	gca Ala	cag Gln	384
ctt Leu	ggg Gly 130	ata Ile	cag Gln	ggc Gly	gtt Val	act Thr 135	gat Asp	gaa Glu	aat Asn	gca Ala	aaa Lys 140	aaa Lys	gct Ala	att Ile	tta Leu	432
aaa Lys 145	gca Ala	aat Asn	gca Ala	gcg Ala	ggg Gly 150	aaa Lys	gat Asp	aag Lys	ggc Gly	gtt Val 155	gaa Glu	gaa Glu	ctt Leu	gaa Glu	aag Lys 160	480
ttg Leu	tcc Ser	gga Gly	tca Ser	tta Leu 165	gaa Glu	agc Ser	tta Leu	tca Ser	aaa Lys 170	gca Ala	gct Ala	aaa Lys	gag Glu	atg Met 175	ctt Leu	528
gct Ala	aat Asn	tca Ser	gtt Val 180	aaa Lys	gag Glu	ctt Leu	aca Thr	agc Ser 185	cct Pro	gtt Val	gtc Val	cat His	ggg Gly 190	aat Asn	aat Asn	576
tca Ser	ggg Gly	aaa Lys 195	gat Asp	ggg Gly	aat Asn	aca Thr	tct Ser 200	gca Ala	aat Asn	tct Ser	gct Ala	gat Asp 205	gag Glu	tct Ser	gtt Val	624
aaa Lys	ggg Gly 210	cct Pro	aat Asn	ctt Leu	aca Thr	gaa Glu 215	ata Ile	agt Ser	aaa Lys	aaa Lys	att Ile 220	aca Thr	gaa Glu	tct Ser	aac Asn	672
gca Ala 225	gtt Val	gtt Val	ctc Leu	gcc Ala	gtg Val 230	aaa Lys	gaa Glu	gtt Val	gaa Glu	act Thr 235	ttg Leu	ctt Leu	aca Thr	tct Ser	ata Ile 240	720

gat gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt 768
 Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser
 245 250 255

tta gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat 816
 Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr
 260 265 270

tta att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca 864
 Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser
 275 280 285

gga gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa 912
 Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu
 290 295 300

ttt act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc 960
 Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly
 305 310 315 320

gtt act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat 1008
 Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp
 325 330 335

aaa act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa 1056
 Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys
 340 345 350

aac ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag 1104
 Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu
 355 360 365

ctt aca agc
 Leu Thr Ser 1113
 370

<210> 34
 <211> 370
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<400> 34
 Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
 1 5 10 15
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
 20 25 30
 Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
 35 40 45
 Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys
 50 55 60
 Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu
 65 70 75 80
 Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys
 85 90 95

Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys Lys
 100 105 110
 Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu
 115 120 125
 Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys
 130 135 140
 Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu
 145 150 155 160
 Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn Ser
 180 185 190
 Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
 195 200 205
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
 210 215 220
 Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp
 225 230 235 240
 Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu
 245 250 255
 Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu
 260 265 270
 Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly
 275 280 285
 Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe
 290 295 300
 Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val
 305 310 315 320
 Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys
 325 330 335
 Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn
 340 345 350
 Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu
 355 360 365
 Thr Ser
 370

<210> 35
 <211> 1112
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OSpC Chimera

<221> CDS
 <222> (1)...(1112)

<400> 35
 atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15

 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

att Ile	acg Thr	gat Asp 35	tct Ser	aat Asn	gcg Ala	gtt Val	tta Leu 40	ctt Leu	gct Ala	gtg Val	aaa Lys	gag Glu 45	gtt Val	gaa Glu	gcg Ala	144
ttg Leu	ctg Leu 50	tca Ser	tct Ser	ata Ile	gat Asp	gag Glu 55	ctt Leu	gct Ala	aaa Lys	gct Ala	att Ile 60	ggt Gly	aaa Lys	aaa Lys	ata Ile	192
aaa Lys 65	aac Asn	gat Asp	ggt Gly	agt Ser	tta Leu 70	gat Asp	aat Asn	gaa Glu	gca Ala	aat Asn 75	cgc Arg	aac Asn	gag Glu	tca Ser	ttg Leu 80	240
tta Leu	gca Ala	gga Gly	gct Ala	tat Tyr 85	aca Thr	ata Ile	tca Ser	acc Thr	tta Leu 90	ata Ile	aca Thr	caa Gln	aaa Lys	tta Leu 95	agt Ser	288
aaa Lys	tta Leu	aac Asn 100	gga Gly	tca Ser	gaa Glu	ggt Gly	tta Leu 105	aag Glu	gaa Glu	aag Lys	att Ile	gcc Ala 110	gca Ala	gct Ala	aag Lys	336
aaa Lys	tgc Cys 115	tct Ser	gaa Glu	gag Glu	ttt Phe	agt Ser	act Thr 120	aaa Lys	cta Leu	aaa Lys	gat Asp 125	aat Asn	cat His	gca Ala	cag Gln	384
ctt Leu	ggt Gly 130	ata Ile	cag Gln	ggc Gly	gtt Val	act Thr 135	gat Asp	gaa Glu	aat Asn	gca Ala 140	aaa Lys	aaa Lys	gct Ala	att Ile	tta Leu	432
aaa Lys 145	gca Ala	aat Asn	gca Ala	gcg Ala	ggt Gly 150	aaa Lys	gat Asp	aag Lys	ggc Gly 155	gtt Val 155	gaa Glu	gaa Glu	ctt Leu	gaa Glu	aag Lys 160	480
ttg Leu	tcc Ser	gga Gly	tca Ser	tta Leu 165	gaa Glu	agc Ser	tta Leu	tca Ser	aaa Lys 170	gca Ala	gct Ala	aaa Lys	gag Glu	atg Met 175	ctt Leu	528
gct Ala	aat Asn	tca Ser 180	gtt Val	aaa Lys	gag Glu	ctt Leu	aca Thr	agc Ser 185	cct Pro	gtt Val	gtc Val	cat His	ggt Gly 190	aat Asn	aat Asn	576
tca Ser	gga Gly	aaa Lys 195	gat Asp	ggg Gly	aat Asn	aca Thr	tct Ser 200	gca Ala	aat Asn	tct Ser	gct Ala 205	gat Asp	gag Glu	tct Ser	gtt Val	624
aaa Lys	ggg Gly 210	cct Pro	aat Asn	ctt Leu	aca Thr	gaa Glu 215	ata Ile	agt Ser	aaa Lys	aaa Lys	att Ile 220	aca Thr	gaa Glu	tct Ser	aac Asn	672
gca Ala 225	gtt Val	gtt Val	ctg Leu	gct Ala	gtg Val 230	aaa Lys	gaa Glu	att Ile	gaa Glu	act Thr 235	ttg Leu	ctt Leu	gca Ala	tct Ser	ata Ile 240	720
gat Asp	gaa Glu	ctt Leu	gct Ala	act Thr 245	aaa Lys	gct Ala	att Ile	ggt Gly	aaa Lys 250	aaa Lys	ata Ile	caa Gln	caa Gln	aat Asn 255	ggt Gly	768
ggt Gly	tta Leu	gct Ala	gtc Val 260	gaa Glu	gcg Ala	ggg Gly	cat His 265	aat Asn	gga Gly	aca Thr	ttg Leu	tta Leu	gca Ala 270	ggt Gly	gct Ala	816

tat aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat 864
 Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn
 275 280 285
 tca gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa 912
 Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu
 290 295 300
 gat ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa 960
 Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu
 305 310 315 320
 aat gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca 1008
 Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala
 325 330 335
 gct aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta 1056
 Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val
 340 345 350
 gaa aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa 1104
 Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys
 355 360 365
 gag ctt ac 1112
 Glu Leu
 370

<210> 36
 <211> 369
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<400> 36
 Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
 1 5 10 15
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
 20 25 30
 Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
 35 40 45
 Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys
 50 55 60
 Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu
 65 70 75 80
 Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys
 85 90 95
 Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys Lys
 100 105 110
 Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu
 115 120 125
 Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys
 130 135 140
 Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu
 145 150 155 160

Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn Ser
 180 185 190
 Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
 195 200 205
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
 210 215 220
 Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp
 225 230 235 240
 Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly
 245 250 255
 Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr
 260 265 270
 Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser
 275 280 285
 Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp
 290 295 300
 Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn
 305 310 315 320
 Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala
 325 330 335
 Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu
 340 345 350
 Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu
 355 360 365
 Leu

<210> 37
 <211> 1106
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OSpC Chimera

<221> CDS
 <222> (1)...(1106)

<400> 37
 atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct 48
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
 1 5 10 15

 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

 att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
 35 40 45

 tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 50 55 60

ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg	240
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu	
65 70 75 80	
tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat	288
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn	
85 90 95	
gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa	336
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln	
100 105 110	
tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt	384
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu	
115 120 125	
ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa	432
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys	
130 135 140	
aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt	480
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe	
145 150 155 160	
aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat	528
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn	
165 170 175	
gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca aga	576
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg	
180 185 190	
aaa gat ggg aat gca tct aca aat tct gcc gat gag tct gtt aaa ggg	624
Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly	
195 200 205	
cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt	672
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val	
210 215 220	
gtt ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa	720
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu	
225 230 235 240	
ctt gct acc aaa gct att ggt aag aaa ata ggc aat aat ggt tta gag	768
Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu	
245 250 255	
gcc aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata	816
Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile	
260 265 270	
tct gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta	864
Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu	
275 280 285	
aag gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat	912
Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn	
290 295 300	

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aaa cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat 960
Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp
305                               310                               315                               320

gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag 1008
Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys
                               325                               330                               335

ggt gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca 1056
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser
                               340                               345                               350

aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt 1104
Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser
                               355                               360                               365

cc 1106

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<210> 38
<211> 368
<212> PRT
<213> Artificial Sequence

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<220>
<223> OspC Chimera

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<400> 38
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
 1      5      10      15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20      25      30
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
 35      40      45
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 50      55      60
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
 65      70      75      80
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
 85      90      95
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
100      105      110
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
115      120      125
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
130      135      140
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
145      150      155      160
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
165      170      175
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg
180      185      190
Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly
195      200      205
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
210      215      220
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu
225      230      235      240

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<210> 39
<211> 1107
<212> DNA
<213> Artificial Sequence
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<221> CDS
<222> (1)...(1107)

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Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser																		
1 5 10 15																		
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa	96																	
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys																		
20 25 30																		
att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc	144																	
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr																		
35 40 45																		
tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa	192																	
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys																		
50 55 60																		
ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg	240																	
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu																		
65 70 75 80																		
tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat	288																	
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn																		
85 90 95																		
gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa	336																	
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln																		
100 105 110																		

tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt	384
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu	
115 120 125	
ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa	432
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys	
130 135 140	
aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt	480
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe	
145 150 155 160	
aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat	528
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn	
165 170 175	
gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca ggg	576
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly	
180 185 190	
aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg	624
Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly	
195 200 205	
cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt	672
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val	
210 215 220	
gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag	720
Val Leu Ala Val Lys Glu Val Glu Thr Leu Thr Ser Ile Asp Glu	
225 230 235 240	
ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat	768
Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp	
245 250 255	
aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta att	816
Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile	
260 265 270	
tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa	864
Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu	
275 280 285	
ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act	912
Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr	
290 295 300	
gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act	960
Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr	
305 310 315 320	
gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act	1008
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr	
325 330 335	
aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg	1056
Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu	
340 345 350	

tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca 1104
 Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr
 355 360 365

agc 1107
 Ser

<210> 40
 <211> 368
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<400> 40
 Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser Ala
 1 5 10 15
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
 20 25 30
 Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu
 35 40 45
 Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile
 50 55 60
 Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu
 65 70 75 80
 Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val
 85 90 95
 Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys
 100 105 110
 Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly
 115 120 125
 Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys
 130 135 140
 His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys
 145 150 155 160
 Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala
 165 170 175
 Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly Lys
 180 185 190
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 195 200 205
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
 210 215 220
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu
 225 230 235 240
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn
 245 250 255
 Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser
 260 265 270
 Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu
 275 280 285
 Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala
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 Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 305 310 315 320

006750-54236550

<400>	41															
atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct	48															
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser																
1 5 10 15																
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa	96															
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys																
20 25 30																
att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc	144															
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr																
35 40 45																
tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa	192															
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys																
50 55 60																
ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg	240															
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu																
65 70 75 80																
tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat	288															
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn																
85 90 95																
gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa	336															
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln																
100 105 110																
tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt	384															
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu																
115 120 125																
ggg ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa	432															
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys																
130 135 140																

aaa Lys 145	cat His	gca Ala	aat Asn	aaa Lys	gat Asp 150	aag Lys	ggg Gly	gct Ala	gca Ala	gaa Glu 155	ctt Leu	gaa Glu	aag Lys	tta Leu	ttt Phe 160	480
aaa Lys	gcg Ala	gta Val	gaa Glu	aac Asn 165	tta Leu	tca Ser	aaa Lys	gca Ala	gct Ala 170	caa Gln	gac Asp	aca Thr	tta Leu	aaa Lys 175	aat Asn	528
gct Ala	gtt Val	aaa Lys	gag Glu 180	ctt Leu	aca Thr	agt Ser	cct Pro	att Ile 185	gtc Val	cat His	ggg Gly	aat Asn 190	aat Asn	tca Ser	gga Gly	576
aaa Lys	gat Asp	ggg Gly 195	aat Asn	aca Thr	tct Ser	gca Ala	aat Asn 200	tct Ser	gct Ala	gat Asp	gag Glu	tct Ser 205	gtt Val	aaa Lys	ggg Gly	624
cct Pro	aat Asn 210	ctt Leu	aca Thr	gaa Glu	ata Ile	agt Ser 215	aaa Lys	aaa Lys	att Ile	aca Thr	gaa Glu 220	tct Ser	aac Asn	gca Ala	gtt Val	672
gtt Val 225	ctg Leu	gct Ala	gtg Val	aaa Lys	gaa Glu 230	att Ile	gaa Glu	act Thr	ttg Leu 235	ctt Leu	gca Ala	tct Ser	ata Ile	gat Asp	gaa Glu 240	720
ctt Leu	gct Ala	act Thr	aaa Lys	gct Ala 245	att Ile	ggg Gly	aaa Lys	aaa Lys	ata Ile 250	caa Gln	caa Gln	aat Asn	ggg Gly 255	ggg Gly	tta Leu	768
gct Ala	gtc Val	gaa Glu	gcg Ala 260	ggg Gly	cat His	aat Asn	gga Gly	aca Thr 265	ttg Leu	tta Leu	gca Ala	ggg Gly 270	gct Ala	tat Tyr	aca Thr	816
ata Ile	tca Ser	aaa Lys 275	cta Leu	ata Ile	aca Thr	caa Gln	aaa Lys 280	tta Leu	gat Asp	gga Gly	ttg Leu	aaa Lys 285	aat Asn	tca Ser	gaa Glu	864
aaa Lys	tta Leu 290	aag Lys	gaa Glu	aaa Lys	att Ile	gaa Glu 295	aat Asn	gct Ala	aag Lys	aaa Lys	tgt Cys 300	tct Ser	gaa Glu	gat Asp	ttt Phe	912
act Thr 305	aaa Lys	aaa Lys	cta Leu	gaa Glu	gga Gly 310	gaa Glu	cat His	gcg Ala	caa Gln	ctt Leu 315	gga Gly	att Ile	gaa Glu	aat Asn	gtt Val 320	960
act Thr	gat Asp	gag Glu	aat Asn	gca Ala 325	aaa Lys	aaa Lys	gct Ala	att Ile	tta Leu 330	ata Ile	aca Thr	gat Asp	gca Ala	gct Ala 335	aaa Lys	1008
gat Asp	aag Lys	ggc Gly	gct Ala 340	gca Ala	gag Glu	ctt Leu	gaa Glu	aag Lys 345	cta Leu	ttt Phe	aaa Lys	gca Ala	gta Val 350	gaa Glu	aac Asn	1056
ttg Leu	gca Ala	aaa Lys 355	gca Ala	gct Ala	aaa Lys	gag Glu	atg Met 360	ctt Leu	gct Ala	aat Asn	tca Ser	gtt Val 365	aaa Lys	gag Glu	ctt Leu	1104
ac																1106
<210> 42																

<400> 42

$\langle 210 \rangle$	43
$\langle 211 \rangle$	633
$\langle 212 \rangle$	DNA

<213> *Borrelia burgdorferi*

<220>

<221> CDS

<222> (1)...(633)

<400> 43

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Met	Lys	Lys	Asn	Thr	Leu	Ser	Ala	Ile	Leu	Met	Thr	Leu	Phe	Leu	Phe	
1				5					10					15		
ata	tct	tgt	aat	aat	tca	ggg	aaa	gat	ggg	aat	aca	tct	gca	aat	tct	96
Ile	Ser	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	
			20					25					30			
gct	gat	gag	tct	gtt	aaa	ggg	cct	aat	ctt	aca	gaa	ata	aat	aaa	aaa	144
Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Asn	Lys	Lys	
		35					40					45				
att	acg	gat	tct	aat	gcg	gtt	tta	ctt	gct	gtg	aaa	gag	gtt	gaa	gcg	192
Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	
	50					55					60					
ttg	ctg	tca	tct	ata	gat	gaa	att	gct	gct	aaa	gct	att	ggt	aaa	aaa	240
Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile	Ala	Ala	Lys	Ala	Ile	Gly	Lys	Lys	
65				70						75					80	
ata	cac	caa	aat	aat	ggt	ttg	gat	acc	gaa	aat	aat	cac	aat	gga	tca	288
Ile	His	Gln	Asn	Asn	Gly	Leu	Asp	Thr	Glu	Asn	Asn	His	Asn	Gly	Ser	
			85					90						95		
ttg	tta	gcg	gga	gct	tat	gca	ata	tca	acc	cta	ata	aaa	caa	aaa	tta	336
Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu	
			100					105					110			
gat	gga	ttg	aaa	aat	gaa	gga	tta	aag	gaa	aaa	att	gat	gcg	gct	aag	384
Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu	Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys	
		115					120					125				
aaa	tgt	tct	gaa	aca	ttt	act	aat	aaa	tta	aaa	gaa	aaa	cac	aca	gat	432
Lys	Cys	Ser	Glu	Thr	Phe	Thr	Asn	Lys	Leu	Lys	Glu	Lys	His	Thr	Asp	
	130					135					140					
ctt	ggt	aaa	gaa	ggt	gtt	act	gat	gct	gat	gca	aaa	gaa	gcc	att	tta	480
Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu	
145					150					155					160	
aaa	gca	aat	ggt	act	aaa	act	aaa	ggt	gct	gaa	gaa	ctt	gga	aaa	tta	528
Lys	Ala	Asn	Gly	Thr	Lys	Thr	Lys	Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu	
			165					170						175		
ttt	gaa	tca	gta	gag	gtc	ttg	tca	aaa	gca	gct	aaa	gag	atg	ctt	gct	576
Phe	Glu	Ser	Val	Glu	Val	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	
			180					185					190			
aat	tca	gtt	aaa	gag	ctt	aca	agc	cct	gtt	gtg	gca	gaa	agt	cca	aaa	624
Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	
		195					200					205				

00596746-061000

aaa cct taa
Lys Pro *
210

633

<210> 44
<211> 209
<212> PRT
<213> *Borrelia burgdorferi*

<400> 44
Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe Ile
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Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
20 25 30
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys Ile
35 40 45
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
50 55 60
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
65 70 75 80
His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser Leu
85 90 95
Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp
100 105 110
Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys
115 120 125
Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu
130 135 140
Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys
145 150 155 160
Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe
165 170 175
Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn
180 185 190
Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys
195 200 205
Pro

<210> 45
<211> 580
<212> DNA
<213> *Borrelia burgdorferi*

<220>
<221> CDS
<222> (1)...(580)

<400> 45
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Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
20 25 30

006745-01000

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45
 ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60
 ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
 65 70 75 80
 ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85 90 95
 gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110
 aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125
 ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140
 aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
 Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
 145 150 155 160
 ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca tcc 576
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ser
 180 185 190
 atg g 580
 Met

<210> 46
 <211> 192
 <212> PRT
 <213> *Borrelia burgdorferi*

<400> 46
 Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
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 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys Ile
 20 25 30
 Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
 35 40 45
 Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
 50 55 60

His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser Leu
 65 70 75 80
 Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp
 85 90 95
 Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys
 100 105 110
 Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu
 115 120 125
 Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys
 130 135 140
 Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe
 145 150 155 160
 Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn
 165 170 175
 Ser Val Lys Glu Leu Thr Ser Pro Val Ala Glu Ser Pro Ser Met
 180 185 190

<210> 47
 <211> 639
 <212> DNA
 <213> *Borrelia garinii*

<220>
 <221> CDS
 <222> (1)...(639)

<400> 47
 atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt 48
 Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe
 1 5 10 15
 ata tct tgt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat 96
 Ile Ser Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn
 20 25 30
 cct gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa 144
 Pro Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
 35 40 45
 aaa att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag 192
 Lys Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu
 50 55 60
 act ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa 240
 Thr Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln
 65 70 75 80
 aaa ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga 288
 Lys Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly
 85 90 95
 tcg ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa 336
 Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys
 100 105 110
 ttg agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag 384
 Leu Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys
 115 120 125

09556746-051900

gct aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat 432
 Ala Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His
 130 135 140

gca gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct 480
 Ala Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala
 145 150 155 160

att tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa 528
 Ile Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys
 165 170 175

gat tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca 576
 Asp Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala
 180 185 190

cta act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt 624
 Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser
 195 200 205

cca aaa aaa cct taa 639
 Pro Lys Lys Pro *
 210

<210> 48
 <211> 211
 <212> PRT
 <213> Borrelia garinii

<400> 48
 Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe Ile
 1 5 10 15
 Ser Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro
 20 25 30
 Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 35 40 45
 Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
 50 55 60
 Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
 65 70 75 80
 Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
 85 90 95
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
 100 105 110
 Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
 115 120 125
 Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
 130 135 140
 Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
 145 150 155 160
 Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
 165 170 175
 Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
 180 185 190
 Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro
 195 200 205

005790-9452550

Lys Lys Pro
210

<210> 49
<211> 624
<212> DNA
<213> *Borrelia afzelii*

<220>
<221> CDS
<222> (1)...(624)

<400> 49
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Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe
1 5 10 15

ata tct tgt aat aat tca ggt ggg gat tct gca tct act aat cct gat 96
Ile Ser Cys Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp
20 25 30

gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa att aca 144
Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr
35 40 45

gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt 192
Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu
50 55 60

tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat 240
Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn
65 70 75 80

gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg ata gca 288
Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala
85 90 95

gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt gta ttg 336
Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu
100 105 110

aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat tgt tcc 384
Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser
115 120 125

caa aaa ttt act act aag cta aaa gat agt cat gca gag ctt ggt ata 432
Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile
130 135 140

caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa aca cat 480
Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His
145 150 155 160

gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca 528
Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser
165 170 175

005790-97235560

51/102

cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat tca gtt 576
 Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val
 180 185 190

aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa cct taa 624
 Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro *
 195 200 205

<210> 50
 <211> 206
 <212> PRT
 <213> Borrelia afzelii

<400> 50
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 Ser Cys Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu
 20 25 30
 Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp
 35 40 45
 Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser
 50 55 60
 Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp
 65 70 75 80
 Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly
 85 90 95
 Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn
 100 105 110
 Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln
 115 120 125
 Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln
 130 135 140
 Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly
 145 150 155 160
 Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu
 165 170 175
 Glu Ser Leu Ser Lys Ala Ala Gln Ala Leu Thr Asn Ser Val Lys
 180 185 190
 Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro
 195 200 205

<210> 51
 <211> 1680
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1680)

<400> 51
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 1 5 10 15

006750-94496550

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa	96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg	144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa	192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys	
50 55 60	
ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca	240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser	
65 70 75 80	
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta	288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu	
85 90 95	
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag	336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	
100 105 110	
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat	384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
115 120 125	
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta	432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130 135 140	
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta	480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145 150 155 160	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct	528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala	
180 185 190	
atg ggt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat cct	624
Met Gly Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro	
195 200 205	
gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa	672
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
210 215 220	
att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act	720
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr	
225 230 235 240	
ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa	768
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys	
245 250 255	

ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg 816
 Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
 260 265 270

ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg 864
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
 275 280 285

agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct 912
 Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
 290 295 300

aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca 960
 Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
 305 310 315 320

gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att 1008
 Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
 325 330 335

tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat 1056
 Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
 340 345 350

tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta 1104
 Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
 355 360 365

act aat tca gtt aaa gaa ctt ggt cac cgt aat aat tca ggt ggg gat 1152
 Thr Asn Ser Val Lys Glu Leu Gly His Arg Asn Asn Ser Gly Gly Asp
 370 375 380

tct gca tct act aat cct gat gag tct gca aaa gga cct aat ctt acc 1200
 Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr
 385 390 395 400

gta ata agc aaa aaa att aca gat tct aat gca ttt tta ctg gct gtg 1248
 Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val
 405 410 415

aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt tct aaa gct 1296
 Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala
 420 425 430

att ggt aaa aaa ata aaa aat gat ggt act tta gat aac gaa gca aat 1344
 Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn
 435 440 445

cga aac gaa tca ttg ata gca gga gct tat gaa ata tca aaa cta ata 1392
 Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile
 450 455 460

aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag aaa aaa att 1440
 Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile
 465 470 475 480

006790-24236550

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<210> 52
<211> 560
<212> PRT
<213> ospC Chimera

<400> 52
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Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
          25          30          35          40          45
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
          50          55          60          65          70
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
          75          80          85          90          95
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
          100          105          110          115          120
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
          125          130          135          140          145
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
          150          155          160          165          170
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
          175          180          185          190          195
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
          200          205          210          215          220
Lys Thr Asn Gly Thr Lys Lys Gly Ala Glu Glu Leu Gly Lys Leu
          225          230          235          240          245
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
          250          255          260          265          270
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala
          275          280          285          290          295
Met Gly Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro
          300          305          310          315          320
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
          325          330          335          340          345
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
          350          355          360          365          370

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<400>	52															
Met	Ala	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	
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Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	
			20					25					30			
Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	
		35					40					45				
Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile	Ala	Ala	Lys	Ala	Ile	Gly	Lys	Lys	
	50					55					60					
Ile	His	Gln	Asn	Asn	Gly	Leu	Asp	Thr	Glu	Tyr	Asn	His	Asn	Gly	Ser	
65					70					75					80	
Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu	
				85					90					95		
Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu	Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys	
			100					105					110			
Lys	Cys	Ser	Glu	Thr	Phe	Thr	Asn	Lys	Leu	Lys	Glu	Lys	His	Thr	Asp	
		115					120					125				
Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu	
	130					135					140					
Lys	Thr	Asn	Gly	Thr	Lys	Thr	Lys	Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu	
145					150					155					160	
Phe	Glu	Ser	Val	Glu	Val	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	
				165					170					175		
Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	Val	Val	Ala	Glu	Ser	Pro	Ala	
			180					185					190			
Met	Gly	Ser	Asn	Ser	Gly	Lys	Gly	Gly	Asp	Ser	Ala	Ser	Thr	Asn	Pro	
		195					200					205				
Ala	Asp	Glu	Ser	Ala	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	
	210					215					220					
Ile	Thr	Asp	Ser	Asn	Ala	Phe	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	
225					230					235					240	

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<210> 53
<211> 1137
<212> DNA
<213> ospC Chimera
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<400> 53																	
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Met	Ala	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser		
1				5					10					15			
gct	gat	gag	tct	gtt	aaa	ggg	cct	aat	ctt	aca	gaa	ata	agt	aaa	aaa	96	
Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys		
			20					25					30				

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192
 Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
 50 55 60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240
 Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 65 70 75 80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288
 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
 85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336
 Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
 100 105 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384
 Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
 115 120 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432
 Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
 130 135 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480
 Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
 145 150 155 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528
 Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
 165 170 175

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat 576
 Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
 180 185 190

tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga 624
 Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly
 195 200 205

cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt 672
 Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
 210 215 220

tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa 720
 Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu
 225 230 235 240

ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat 768
 Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp
 245 250 255

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aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata 816
Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile
260 265 270

tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta 864
Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu
275 280 285

aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act 912
Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr
290 295 300

aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat 960
Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp
305 310 315 320

gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag 1008
Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys
325 330 335

ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca 1056
Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser
340 345 350

aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat 1104
Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn
355 360 365

cct gtt gtg gca gaa agt cca aaa aaa cct taa 1137
Pro Val Val Ala Glu Ser Pro Lys Lys Pro *
370 375

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<210> 54
<211> 378
<212> PRT
<213> ospC Chimera

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20 25 30
Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala
35 40 45
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
65 70 75 80
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
85 90 95
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys
100 105 110
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
115 120 125
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
130 135 140
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
145 150 155 160

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Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
 165 170 175
 Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
 180 185 190
 Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly
 195 200 205
 Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
 210 215 220
 Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu
 225 230 235 240
 Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp
 245 250 255
 Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile
 260 265 270
 Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu
 275 280 285
 Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr
 290 295 300
 Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp
 305 310 315 320
 Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys
 325 330 335
 Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser
 340 345 350
 Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn
 355 360 365
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro
 370 375

<210> 55
 <211> 1158
 <212> DNA
 <213> ospC Chimera

<220>
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 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30
 att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45
 ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60
 ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
 65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta	288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu	
85 90 95	
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag	336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	
100 105 110	
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat	384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
115 120 125	
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta	432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130 135 140	
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta	480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145 150 155 160	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct	528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys	
180 185 190	
aaa cct ttc cat ggt aat aat tca ggt ggg gat tct gca tct act aat	624
Lys Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn	
195 200 205	
cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa	672
Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys	
210 215 220	
att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct	720
Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala	
225 230 235 240	
ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata	768
Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile	
245 250 255	
aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg	816
Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu	
260 265 270	
ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt	864
Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser	
275 280 285	
gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat	912
Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp	
290 295 300	

tgt	tcc	caa	aaa	ttt	act	act	aag	cta	aaa	gat	agt	cat	gca	gag	ctt	960
Cys	Ser	Gln	Lys	Phe	Thr	Thr	Lys	Leu	Lys	Asp	Ser	His	Ala	Glu	Leu	
305					310					315					320	
ggt	ata	caa	agc	gtt	cag	gat	gat	aat	gca	aaa	aaa	gct	att	tta	aaa	1008
Gly	Ile	Gln	Ser	Val	Gln	Asp	Asp	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	
				325					330					335		
aca	cat	gga	act	aaa	gac	aag	ggt	gct	aaa	gaa	ctt	gaa	gag	tta	ttt	1056
Thr	His	Gly	Thr	Lys	Asp	Lys	Gly	Ala	Lys	Glu	Leu	Glu	Glu	Leu	Phe	
			340					345					350			
aaa	tca	cta	gaa	agc	ttg	tca	aaa	gca	gcg	caa	gca	gca	tta	act	aat	1104
Lys	Ser	Leu	Glu	Ser	Leu	Ser	Lys	Ala	Ala	Gln	Ala	Ala	Leu	Thr	Asn	
		355					360					365				
tca	gtt	aaa	gag	ctt	aca	aat	cct	gtt	gtg	gca	gaa	agt	cca	aaa	aaa	1152
Ser	Val	Lys	Glu	Leu	Thr	Asn	Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	Lys	
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cct	taa															1158
Pro	*															
385																

<210> 56
 <211> 384
 <212> PRT
 <213> ospC Chimera

<400> 56

Ala	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	
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Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	
			20					25					30			
Thr	Asp	Ser	Asn	Ala	Val	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	
		35				40					45					
Leu	Ser	Ser	Ile	Asp	Glu	Ile	Ala	Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	
	50				55						60					
His	Gln	Asn	Asn	Gly	Leu	Asp	Thr	Glu	Tyr	Asn	His	Asn	Gly	Ser	Leu	
65				70				75							80	
Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu	Asp	
			85					90					95			
Gly	Leu	Lys	Asn	Glu	Gly	Leu	Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys	Lys	
			100					105				110				
Cys	Ser	Glu	Thr	Phe	Thr	Asn	Lys	Leu	Lys	Glu	Lys	His	Thr	Asp	Leu	
		115				120						125				
Gly	Lys	Glu	Gly	Val	Thr	Asp	Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu	Lys	
	130				135						140					
Thr	Asn	Gly	Thr	Lys	Thr	Lys	Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu	Phe	
145				150					155						160	
Glu	Ser	Val	Glu	Val	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	
			165					170					175			
Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	Lys	
		180						185					190			
Pro	Phe	His	Gly	Asn	Asn	Ser	Gly	Gly	Asp	Ser	Ala	Ser	Thr	Asn	Pro	
	195					200					205					
Asp	Glu	Ser	Ala	Lys	Gly	Pro	Asn	Leu	Thr	Val	Ile	Ser	Lys	Lys	Ile	
	210					215					220					


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Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu
225                230                235                240
Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys
                245                250                255
Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile
                260                265                270
Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val
                275                280                285
Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys
                290                295                300
Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly
305                310                315                320
Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr
                325                330                335
His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys
                340                345                350
Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser
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Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro
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<210> 57
<211> 1161
<212> DNA
<213> ospC Chimera

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<221> CDS
<222> (1)...(1161)

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Met Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro
  1                5                10                15

gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa      96
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
                20                25                30

att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act     144
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
                35                40                45

ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa     192
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
                50                55                60

ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg     240
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
                65                70                75                80

ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg     288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
                85                90                95

agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct     336
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
                100                105                110

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aag	aaa	tgt	tcc	gaa	gaa	ttt	act	aat	aaa	cta	aaa	agt	ggt	cat	gca	384
Lys	Lys	Cys	Ser	Glu	Glu	Phe	Thr	Asn	Lys	Leu	Lys	Ser	Gly	His	Ala	
		115					120					125				
gat	ctt	ggc	aaa	cag	gat	gct	acc	gat	gat	cat	gca	aaa	gca	gct	att	432
Asp	Leu	Gly	Lys	Gln	Asp	Ala	Thr	Asp	Asp	His	Ala	Lys	Ala	Ala	Ile	
	130					135					140					
tta	aaa	aca	cat	gca	act	acc	gat	aaa	ggt	gct	aaa	gaa	ttt	aaa	gat	480
Leu	Lys	Thr	His	Ala	Thr	Thr	Asp	Lys	Gly	Ala	Lys	Glu	Phe	Lys	Asp	
145					150					155					160	
tta	ttt	gaa	tca	gta	gaa	ggt	ttg	tta	aaa	gca	gct	caa	gta	gca	cta	528
Leu	Phe	Glu	Ser	Val	Glu	Gly	Leu	Leu	Lys	Ala	Ala	Gln	Val	Ala	Leu	
				165					170					175		
act	aat	tca	ggt	aaa	gaa	ctt	aca	agt	cct	ggt	gta	gca	gaa	agt	cca	576
Thr	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	Val	Val	Ala	Glu	Ser	Pro	
			180					185					190			
aaa	aaa	cct	cat	atg	gct	aat	aat	tca	ggt	ggg	gat	tct	gca	tct	act	624
Lys	Lys	Pro	His	Met	Ala	Asn	Asn	Ser	Gly	Gly	Asp	Ser	Ala	Ser	Thr	
		195				200						205				
aat	cct	gat	gag	tct	gca	aaa	gga	cct	aat	ctt	acc	gta	ata	agc	aaa	672
Asn	Pro	Asp	Glu	Ser	Ala	Lys	Gly	Pro	Asn	Leu	Thr	Val	Ile	Ser	Lys	
	210					215					220					
aaa	att	aca	gat	tct	aat	gca	ttt	tta	ctg	gct	gtg	aaa	gaa	ggt	gag	720
Lys	Ile	Thr	Asp	Ser	Asn	Ala	Phe	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	
225					230					235					240	
gct	ttg	ctt	tca	tct	ata	gat	gaa	ctt	tct	aaa	gct	att	ggt	aaa	aaa	768
Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Leu	Ser	Lys	Ala	Ile	Gly	Lys	Lys	
				245					250					255		
ata	aaa	aat	gat	ggt	act	tta	gat	aac	gaa	gca	aat	cga	aac	gaa	tca	816
Ile	Lys	Asn	Asp	Gly	Thr	Leu	Asp	Asn	Glu	Ala	Asn	Arg	Asn	Glu	Ser	
			260					265					270			
ttg	ata	gca	gga	gct	tat	gaa	ata	tca	aaa	cta	ata	aca	caa	aaa	tta	864
Leu	Ile	Ala	Gly	Ala	Tyr	Glu	Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	
		275					280					285				
agt	gta	ttg	aat	tca	gaa	gaa	tta	aag	aaa	aaa	att	aaa	gag	gct	aag	912
Ser	Val	Leu	Asn	Ser	Glu	Glu	Leu	Lys	Lys	Lys	Ile	Lys	Glu	Ala	Lys	
	290					295					300					
gat	tgt	tcc	caa	aaa	ttt	act	act	aag	cta	aaa	gat	agt	cat	gca	gag	960
Asp	Cys	Ser	Gln	Lys	Phe	Thr	Thr	Lys	Leu	Lys	Asp	Ser	His	Ala	Glu	
305					310					315					320	
ctt	ggt	ata	caa	agc	gtt	cag	gat	gat	aat	gca	aaa	aaa	gct	att	tta	1008
Leu	Gly	Ile	Gln	Ser	Val	Gln	Asp	Asp	Asn	Ala	Lys	Lys	Ala	Ile	Leu	
				325					330					335		

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aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta 1056
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
340 345 350

ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act 1104
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
355 360 365

aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa 1152
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
370 375 380

aaa cct taa 1161
Lys Pro *
385

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<210> 58
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<212> PRT
<213> ospC Chimera

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Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
35 40 45
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
50 55 60
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
65 70 75 80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
85 90 95
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
100 105 110
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
115 120 125
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
130 135 140
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
145 150 155 160
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
165 170 175
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro
180 185 190
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr
195 200 205
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys
210 215 220
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu
225 230 235 240
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
245 250 255
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
260 265 270
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
275 280 285

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Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
 290 295 300
 Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
 305 310 315 320
 Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
 325 330 335
 Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
 340 345 350
 Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
 355 360 365
 Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
 370 375 380
 Lys Pro
 385

<210> 59
 <211> 1197
 <212> DNA
 <213> ospC Chimera

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 1 5 10 15
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95
 acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110
 tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125

00596745-061900

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat	432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn	
130 135 140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat	480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp	
145 150 155 160	
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys	
165 170 175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser	
180 185 190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser	
195 200 205	
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca ggg aaa gat	672
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp	
210 215 220	
ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat	720
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn	
225 230 235 240	
ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc	768
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu	
245 250 255	
gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct	816
Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala	
260 265 270	
aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag	864
Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu	
275 280 285	
gca gat cac aac gga tca tta ata tca gga gca tat tta att tca aac	912
Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn	
290 295 300	
tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag	960
Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys	
305 310 315 320	
gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa	1008
Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys	
325 330 335	
tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat	1056
Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp	
340 345 350	
aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc	1104
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<210> 61
<211> 1196
<212> DNA
<213> ospC Chimera
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1				5					10					15		
gca	caa	aaa	ggt	gct	gag	tca	att	gga	tcc	tgt	aat	aat	tca	ggg	aaa	96
Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys	
			20					25					30			
gat	ggg	aat	aca	tct	gca	aat	tct	gct	gat	gag	tct	gtt	aaa	ggg	cct	144
Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	
		35					40					45				
aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	acg	gat	tct	aat	gcg	gtt	tta	192
Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	
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ctt	gct	gtg	aaa	gag	gtt	gaa	gcg	ttg	ctg	tca	tct	ata	gat	gaa	att	240
Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile	
65					70					75					80	
gct	gct	aaa	gct	att	ggg	aaa	aaa	ata	cac	caa	aat	aat	ggg	ttg	gat	288
Ala	Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	His	Gln	Asn	Asn	Gly	Leu	Asp	
				85					90					95		
acc	gaa	tat	aat	cac	aat	gga	tca	ttg	tta	gcg	gga	gct	tat	gca	ata	336
Thr	Glu	Tyr	Asn	His	Asn	Gly	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	
			100					105					110			
tca	acc	cta	ata	aaa	caa	aaa	tta	gat	gga	ttg	aaa	aat	gaa	gga	tta	384
Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu	
		115					120					125				
aag	gaa	aaa	att	gat	gcg	gct	aag	aaa	tgt	tct	gaa	aca	ttt	act	aat	432
Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys	Lys	Cys	Ser	Glu	Thr	Phe	Thr	Asn	
	130					135					140					
aaa	tta	aaa	gaa	aaa	cac	aca	gat	ctt	ggg	aaa	gaa	ggg	gtt	act	gat	480
Lys	Leu	Lys	Glu	Lys	His	Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	
145					150					155					160	

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys	
165 170 175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser	
180 185 190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser	
195 200 205	
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca gga aaa gat	672
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp	
210 215 220	
ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat	720
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn	
225 230 235 240	
ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg	768
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu	
245 250 255	
gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct	816
Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala	
260 265 270	
act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc	864
Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val	
275 280 285	
gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca	912
Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
290 295 300	
aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta	960
Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu	
305 310 315 320	
aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa	1008
Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys	
325 330 335	
aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat	1056
Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp	
340 345 350	
gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag	1104
Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys	
355 360 365	
ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca	1152
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala	
370 375 380	

006745-061900

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 385 390 395

1196

<210> 62
 <211> 397
 <212> PRT
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<400> 62

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 20 25 30
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
 50 55 60
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala
 65 70 75 80
 Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr
 85 90 95
 Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser
 100 105 110
 Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys
 115 120 125
 Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys
 130 135 140
 Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala
 145 150 155 160
 Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly
 165 170 175
 Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys
 180 185 190
 Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
 195 200 205
 Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp Gly
 210 215 220
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
 225 230 235 240
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
 245 250 255
 Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
 260 265 270
 Lys Ala Ile Gly Lys Lys Ile Gln Asn Gly Gly Leu Ala Val Glu
 275 280 285
 Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys
 290 295 300
 Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys
 305 310 315 320
 Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys
 325 330 335
 Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu
 340 345 350
 Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly
 355 360 365

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 385 390 395

<210> 63
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 1 5 10 15
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80
 gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95
 gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 100 105 110
 acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
 115 120 125
 aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432
 Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
 130 135 140
 aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
 145 150 155 160
 gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
 165 170 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180 185 190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195 200 205	
agc cct gtt gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct	672
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser	
210 215 220	
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata	720
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile	
225 230 235 240	
agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa	768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu	
245 250 255	
gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt	816
Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly	
260 265 270	
aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac	864
Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn	
275 280 285	
gga tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa	912
Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys	
290 295 300	
aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa	960
Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu	
305 310 315 320	
aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa	1008
Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu	
325 330 335	
cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa	1056
His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys	
340 345 350	
gcc att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt	1104
Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu	
355 360 365	
gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag	1152
Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu	
370 375 380	
atg ctt act aat tca gtt aaa gag ctt aca agc	1185
Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser	
385 390 395	

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 <213> ospC Chimera

<400> 64

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Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys	Asp
			20					25					30		
Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn
		35					40					45			
Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	Leu
	50					55					60				
Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Leu	Ala
65					70				75					80	
Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn	Asp	Gly	Ser	Leu	Asp	Asn	Glu
				85				90						95	
Ala	Asn	Arg	Asn	Glu	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Thr	Ile	Ser	Thr
			100					105					110		
Leu	Ile	Thr	Gln	Lys	Leu	Ser	Lys	Leu	Asn	Gly	Ser	Glu	Gly	Leu	Lys
	115						120					125			
Glu	Lys	Ile	Ala	Ala	Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe	Ser	Thr	Lys
	130					135					140				
Leu	Lys	Asp	Asn	His	Ala	Gln	Leu	Gly	Ile	Gln	Gly	Val	Thr	Asp	Glu
145					150				155					160	
Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Ala	Asn	Ala	Ala	Gly	Lys	Asp	Lys
				165				170						175	
Gly	Val	Glu	Glu	Leu	Glu	Lys	Leu	Ser	Gly	Ser	Leu	Glu	Ser	Leu	Ser
		180						185				190			
Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser
	195					200						205			
Pro	Val	Val	His	Gly	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala
	210				215						220				
Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser
225					230				235					240	
Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Val
			245					250					255		
Glu	Thr	Leu	Leu	Thr	Ser	Ile	Asp	Glu	Leu	Ala	Lys	Ala	Ile	Gly	Lys
		260						265					270		
Lys	Ile	Lys	Asn	Asp	Val	Ser	Leu	Asp	Asn	Glu	Ala	Asp	His	Asn	Gly
	275						280					285			
Ser	Leu	Ile	Ser	Gly	Ala	Tyr	Leu	Ile	Ser	Asn	Leu	Ile	Thr	Lys	Lys
	290					295				300					
Ile	Ser	Ala	Ile	Lys	Asp	Ser	Gly	Glu	Leu	Lys	Ala	Glu	Ile	Glu	Lys
305				310				315						320	
Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe	Thr	Ala	Lys	Leu	Lys	Gly	Glu	His
			325					330					335		
Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	Asp	Asn	Ala	Lys	Lys	Ala
		340						345				350			
Ile	Leu	Lys	Thr	Asn	Asn	Asp	Lys	Thr	Lys	Gly	Ala	Asp	Glu	Leu	Glu
	355					360					365				
Lys	Leu	Phe	Glu	Ser	Val	Lys	Asn	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met
	370					375					380				
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385					390										

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006790 3423554

<212> DNA
 <213> ospC Chimera

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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys	
1 5 10 15	
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa	96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys	
20 25 30	
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 40 45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50 55 60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu	
65 70 75 80	
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat	288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn	
85 90 95	
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
100 105 110	
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu	
115 120 125	
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr	
130 135 140	
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat	480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp	
145 150 155 160	
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp	
165 170 175	
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180 185 190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195 200 205	

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agc cct gtt gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct 672
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser
210 215 220

gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata 720
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
225 230 235 240

agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa 768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
245 250 255

att gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att 816
Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile
260 265 270

ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat 864
Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His
275 280 285

aat gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca 912
Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr
290 295 300

caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att 960
Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile
305 310 315 320

gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga 1008
Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly
325 330 335

gaa cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa 1056
Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys
340 345 350

aaa gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag 1104
Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu
355 360 365

ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa 1152
Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys
370 375 380

gag atg ctt gct aat tca gtt aaa gag ctt ac 1184
Glu Met Leu Ala Asn Ser Val Lys Glu Leu
385 390

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Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
 20 25 30
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
 50 55 60
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala
 65 70 75 80
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu
 85 90 95
 Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr
 100 105 110
 Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys
 115 120 125
 Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys
 130 135 140
 Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu
 145 150 155 160
 Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys
 165 170 175
 Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
 210 215 220
 Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
 225 230 235 240
 Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile
 245 250 255
 Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly
 260 265 270
 Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn
 275 280 285
 Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln
 290 295 300
 Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu
 305 310 315 320
 Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu
 325 330 335
 His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys
 340 345 350
 Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu
 355 360 365
 Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu
 370 375 380
 Met Leu Ala Asn Ser Val Lys Glu Leu
 385 390

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1				5					10					15		
gca	caa	aaa	ggt	gct	gag	tca	att	gga	tcc	tgt	aat	aat	tca	ggg	aaa	96
Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys	
			20					25					30			
gat	ggg	aat	aca	tct	gca	aat	tct	gct	gat	gag	tct	gtt	aaa	ggg	cct	144
Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	
		35					40					45				
aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	acg	gat	tct	aat	gcg	gtt	tta	192
Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	
	50					55					60					
ctt	gct	gtg	aaa	gag	gtt	gaa	gcg	ttg	ctg	tca	tct	ata	gat	gag	ctt	240
Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Leu	
65					70				75						80	
gct	aaa	gct	att	ggt	aaa	aaa	ata	aaa	aac	gat	ggt	agt	tta	gat	aat	288
Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn	Asp	Gly	Ser	Leu	Asp	Asn	
				85					90					95		
gaa	gca	aat	cgc	aac	gag	tca	ttg	tta	gca	gga	gct	tat	aca	ata	tca	336
Glu	Ala	Asn	Arg	Asn	Glu	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Thr	Ile	Ser	
			100					105					110			
acc	tta	ata	aca	caa	aaa	tta	agt	aaa	tta	aac	gga	tca	gaa	ggt	tta	384
Thr	Leu	Ile	Thr	Gln	Lys	Leu	Ser	Lys	Leu	Asn	Gly	Ser	Glu	Gly	Leu	
		115					120					125				
aag	gaa	aag	att	gcc	gca	gct	aag	aaa	tgc	tct	gaa	gag	ttt	agt	act	432
Lys	Glu	Lys	Ile	Ala	Ala	Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe	Ser	Thr	
	130					135					140					
aaa	cta	aaa	gat	aat	cat	gca	cag	ctt	ggt	ata	cag	ggc	gtt	act	gat	480
Lys	Leu	Lys	Asp	Asn	His	Ala	Gln	Leu	Gly	Ile	Gln	Gly	Val	Thr	Asp	
145					150				155						160	
gaa	aat	gca	aaa	aaa	gct	att	tta	aaa	gca	aat	gca	gcg	ggt	aaa	gat	528
Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Ala	Asn	Ala	Ala	Gly	Lys	Asp	
				165					170					175		
aag	ggc	gtt	gaa	gaa	ctt	gaa	aag	ttg	tcc	gga	tca	tta	gaa	agc	tta	576
Lys	Gly	Val	Glu	Glu	Leu	Glu	Lys	Leu	Ser	Gly	Ser	Leu	Glu	Ser	Leu	
			180					185					190			
tca	aaa	gca	gct	aaa	gag	atg	ctt	gct	aat	tca	gtt	aaa	gag	ctt	aca	624
Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	
		195					200					205				
agc	cct	gtt	gtc	cat	ggt	aat	aat	tca	aga	aaa	gat	ggg	aat	gca	tct	672
Ser	Pro	Val	Val	His	Gly	Asn	Asn	Ser	Arg	Lys	Asp	Gly	Asn	Ala	Ser	
	210					215					220					

006790-94296460

aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata 720
 Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
 225 230 235 240

agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa 768
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
 245 250 255

gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att 816
 Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile
 260 265 270

ggg aag aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac 864
 Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn
 275 280 285

aca tca ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa 912
 Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu
 290 295 300

aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca 960
 Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr
 305 310 315 320

gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat 1008
 Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His
 325 330 335

gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct 1056
 Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala
 340 345 350

att tta aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa 1104
 Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu
 355 360 365

aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca 1152
 Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr
 370 375 380

tta aaa aat gct gtt aaa gag ctt aca agt cc 1184
 Leu Lys Asn Ala Val Lys Glu Leu Thr Ser
 385 390

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 <212> PRT
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 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
 20 25 30
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
 50 55 60

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<222> (1)...(1209)
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1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa	96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys	
20 25 30	
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 40 45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50 55 60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu	
65 70 75 80	
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat	288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn	
85 90 95	
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
100 105 110	
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu	
115 120 125	
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr	
130 135 140	
aaa cta aaa gat aat cat gca cag ctt ggt ata cag gcc gtt act gat	480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp	
145 150 155 160	
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp	
165 170 175	
aag gcc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180 185 190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195 200 205	
agc cct gtt gtc cat ggt aat aat tca ggt ggg gat tct gca tct act	672
Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr	
210 215 220	
aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa	720
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys	
225 230 235 240	
aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag	768
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu	
245 250 255	

gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa 816
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
260 265 270

ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca 864
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
275 280 285

ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta 912
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
290 295 300

agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag 960
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
305 310 315 320

gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag 1008
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
325 330 335

ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta 1056
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
340 345 350

aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta 1104
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
355 360 365

ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act 1152
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
370 375 380

aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa 1200
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
385 390 395 400

aaa cct taa 1209
Lys Pro *

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<211> 401
<212> PRT
<213> ospC Chimera

<400> 70
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
1 5 10 15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
20 25 30
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
35 40 45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
50 55 60
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala
65 70 75 80

005745-057900

Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu
 85 90 95
 Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr
 100 105 110
 Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys
 115 120 125
 Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys
 130 135 140
 Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu
 145 150 155 160
 Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys
 165 170 175
 Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn
 210 215 220
 Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys
 225 230 235 240
 Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala
 245 250 255
 Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile
 260 265 270
 Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 275 280 285
 Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser
 290 295 300
 Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp
 305 310 315 320
 Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu
 325 330 335
 Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys
 340 345 350
 Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe
 355 360 365
 Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn
 370 375 380
 Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys
 385 390 395 400
 Pro

<210> 71
 <211> 1179
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1179)

<400> 71
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa	96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys	
20 25 30	
gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 40 45	
aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val	
50 55 60	
ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt	240
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu	
65 70 75 80	
gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc	288
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala	
85 90 95	
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct	336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser	
100 105 110	
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag	384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys	
115 120 125	
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa	432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys	
130 135 140	
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat	480
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp	
145 150 155 160	
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt	528
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly	
165 170 175	
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa	576
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys	
180 185 190	
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct	624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro	
195 200 205	
att gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct gca aat	672
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn	
210 215 220	
tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa	720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys	
225 230 235 240	
aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa	768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu	
245 250 255	

act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa 816
 Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys
 260 265 270

ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga tca 864
 Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser
 275 280 285

tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa ata 912
 Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile
 290 295 300

agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct 960
 Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala
 305 310 315 320

aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca 1008
 Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr
 325 330 335

gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att 1056
 Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile
 340 345 350

tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag 1104
 Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys
 355 360 365

tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt 1152
 Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu
 370 375 380

act aat tca gtt aaa gag ctt aca agc 1179
 Thr Asn Ser Val Lys Glu Leu Thr Ser
 385 390

<210> 72
 <211> 392
 <212> PRT
 <213> ospC Chimera

<400> 72
 Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
 1 5 10 15
 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
 20 25 30
 Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
 50 55 60
 Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala
 65 70 75 80
 Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn
 85 90 95
 Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp
 100 105 110

005790-94795560

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<210> 73
<211> 1178
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1178)
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<400> 73																
atg	aga	tta	tta	ata	gga	ttt	gct	tta	gcg	tta	gct	tta	ata	gga	tgt	48
Met	Arg	Leu	Leu	Ile	Gly	Phe	Ala	Leu	Ala	Leu	Ala	Leu	Ile	Gly	Cys	
1				5					10					15		
gca	caa	aaa	ggt	gct	gag	tca	att	gga	tcc	tgt	aat	aat	tca	gga	aaa	96
Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys	
			20					25					30			
gat	ggg	aat	gca	tct	gca	aat	tct	gct	gat	gag	tct	gtt	aaa	ggg	cct	144
Asp	Gly	Asn	Ala	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	
		35					40					45				

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val	
50 55 60	
ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt	240
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu	
65 70 75 80	
gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc	288
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala	
85 90 95	
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct	336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser	
100 105 110	
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag	384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys	
115 120 125	
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa	432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys	
130 135 140	
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat	480
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp	
145 150 155 160	
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt	528
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly	
165 170 175	
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa	576
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys	
180 185 190	
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct	624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro	
195 200 205	
att gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct gca aat	672
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn	
210 215 220	
tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa	720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys	
225 230 235 240	
aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa	768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu	
245 250 255	
act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa	816
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys	
260 265 270	

aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga 864
 Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly
 275 280 285
 aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa 912
 Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys
 290 295 300
 tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat 960
 Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn
 305 310 315 320
 gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat 1008
 Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His
 325 330 335
 gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct 1056
 Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala
 340 345 350
 att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa 1104
 Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu
 355 360 365
 aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg 1152
 Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met
 370 375 380
 ctt gct aat tca gtt aaa gag ctt ac 1178
 Leu Ala Asn Ser Val Lys Glu Leu
 385 390

<210> 74
 <211> 391
 <212> PRT
 <213> ospC Chimera

<400> 74
 Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
 1 5 10 15
 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
 20 25 30
 Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
 50 55 60
 Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala
 65 70 75 80
 Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn
 85 90 95
 Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp
 100 105 110
 Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu
 115 120 125
 Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu
 130 135 140
 Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn
 145 150 155 160

00596745-051900

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt	240
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu	
65 70 75 80	
gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc	288
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala	
85 90 95	
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct	336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser	
100 105 110	
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag	384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys	
115 120 125	
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa	432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys	
130 135 140	
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat	480
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp	
145 150 155 160	
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt	528
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly	
165 170 175	
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa	576
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys	
180 185 190	
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct	624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro	
195 200 205	
att gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct aca aat	672
Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn	
210 215 220	
tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa	720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys	
225 230 235 240	
aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag	768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu	
245 250 255	
acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aag	816
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys	
260 265 270	
aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca	864
Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser	
275 280 285	
ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta	912
Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu	
290 295 300	

aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag 960
 Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys
 305 310 315 320

 caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg 1008
 Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val
 325 330 335

 ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta 1056
 Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu
 340 345 350

 aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta 1104
 Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
 355 360 365

 ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa 1152
 Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys
 370 375 380

 aat gct gtt aaa gag ctt aca agt cc 1178
 Asn Ala Val Lys Glu Leu Thr Ser
 385 390

<210> 76
 <211> 391
 <212> PRT
 <213> ospC Chimera

<400> 76
 Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
 1 5 10 15
 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
 20 25 30
 Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
 50 55 60
 Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala
 65 70 75 80
 Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn
 85 90 95
 Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp
 100 105 110
 Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu
 115 120 125
 Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu
 130 135 140
 Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn
 145 150 155 160
 Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala
 165 170 175
 Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala
 180 185 190
 Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile
 195 200 205

Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser
 210 215 220
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 225 230 235 240
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
 245 250 255
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 260 265 270
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
 275 280 285
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
 290 295 300
 Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
 305 310 315 320
 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
 325 330 335
 Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
 340 345 350
 Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
 355 360 365
 Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
 370 375 380
 Ala Val Lys Glu Leu Thr Ser
 385 390

<210> 77
 <211> 1230
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1230)

<400> 77
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 1 5 10 15
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205

cct gtt gtg gca gaa agt cca aaa aaa cct ttc cat ggt aat aat tca 672
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser
 210 215 220

ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga cct 720
 Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro
 225 230 235 240

aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt tta 768
 Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu
 245 250 255

ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt 816
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 260 265 270

tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat aac 864
 Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn
 275 280 285

gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata tca 912
 Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser
 290 295 300

aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag 960
 Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys
 305 310 315 320

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<210> 78
<211> 408
<212> PRT
<213> ospC Chimera
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<400>	78															
Arg 1	Leu	Leu	Ile	Gly 5	Phe	Ala	Leu	Ala	Leu	Ala	Leu	Ile	Gly	Cys 15	Ala	
Gln	Lys	Gly	Ala 20	Glu	Ser	Ile	Gly	Ser 25	Cys	Asn	Asn	Ser	Gly 30	Lys	Asp	
Gly	Asn	Thr 35	Ser	Ala	Asn	Ser	Ala 40	Asp	Glu	Ser	Val	Lys 45	Gly	Pro	Asn	
Leu 50	Thr	Glu	Ile	Ser	Lys	Lys 55	Ile	Thr	Asp	Ser	Asn 60	Ala	Val	Leu	Leu	
Ala 65	Val	Lys	Glu	Val	Glu	Ala 70	Leu	Leu	Ser	Ser 75	Ile	Asp	Glu	Ile	Ala	
Ala	Lys	Ala	Ile	Gly 85	Lys	Lys	Ile	His	Gln 90	Asn	Asn	Gly	Leu	Asp 95	Thr	
Glu	Tyr	Asn	His 100	Asn	Gly	Ser	Leu	Leu 105	Ala	Gly	Ala	Tyr	Ala 110	Ile	Ser	
Thr	Leu	Ile 115	Lys	Gln	Lys	Leu	Asp 120	Gly	Leu	Lys	Asn	Glu 125	Gly	Leu	Lys	
Glu 130	Lys	Ile	Asp	Ala	Ala	Lys 135	Lys	Cys	Ser	Glu	Thr 140	Phe	Thr	Asn	Lys	
Leu 145	Lys	Glu	Lys	His	Thr 150	Asp	Leu	Gly	Lys	Glu 155	Gly	Val	Thr	Asp	Ala	
Asp	Ala	Lys	Glu	Ala 165	Ile	Leu	Lys	Thr	Asn 170	Gly	Thr	Lys	Thr	Lys 175	Gly	
Ala	Glu	Glu	Leu 180	Gly	Lys	Leu	Phe	Glu 185	Ser	Val	Glu	Val	Leu 190	Ser	Lys	
Ala	Ala	Lys 195	Glu	Met	Leu	Ala	Asn 200	Ser	Val	Lys	Glu	Leu 205	Thr	Ser	Pro	
Val	Val 210	Ala	Glu	Ser	Pro	Lys 215	Lys	Pro	Phe	His	Gly 220	Asn	Asn	Ser	Gly	

Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn
 225 230 235 240
 Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu
 245 250 255
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser
 260 265 270
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu
 275 280 285
 Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys
 290 295 300
 Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys
 305 310 315 320
 Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu
 325 330 335
 Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn
 340 345 350
 Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala
 355 360 365
 Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala
 370 375 380
 Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val
 385 390 395 400
 Val Ala Glu Ser Pro Lys Lys Pro
 405

<210> 79
 <211> 1209
 <212> DNA
 <213> ospC Chimera

<220>
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 <222> (1)...(1209)

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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80

 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95

acc Thr	gaa Glu	tat Tyr	aat Asn 100	cac His	aat Asn	gga Gly	tca Ser	ttg Leu 105	tta Leu	gcg Ala	gga Gly	gct Ala	tat Tyr 110	gca Ala	ata Ile	336
tca Ser	acc Thr	cta Leu 115	ata Ile	aaa Lys	caa Gln	aaa Lys	tta Leu 120	gat Asp	gga Gly	ttg Leu	aaa Lys	aat Asn 125	gaa Glu	gga Gly	tta Leu	384
aag Lys	gaa Glu 130	aaa Lys	att Ile	gat Asp	gcg Ala	gct Ala 135	aag Lys	aaa Lys	tgt Cys	tct Ser	gaa Glu 140	aca Thr	ttt Phe	act Thr	aat Asn	432
aaa Lys 145	tta Leu	aaa Lys	gaa Glu	aaa Lys	cac His 150	aca Thr	gat Asp	ctt Leu	ggt Gly	aaa Lys 155	gaa Glu	ggt Gly	gtt Val	act Thr	gat Asp 160	480
gct Ala	gat Asp	gca Ala	aaa Lys	gaa Glu 165	gcc Ala	att Ile	tta Leu	aaa Lys	aca Thr 170	aat Asn	ggt Gly	act Thr	aaa Lys	act Thr 175	aaa Lys	528
ggt Gly	gct Ala	gaa Glu 180	gaa Glu	ctt Leu	gga Gly	aaa Lys	tta Leu	ttt Phe 185	gaa Glu	tca Ser	gta Val	gag Glu 190	gtc Val	ttg Leu	tca Ser	576
aaa Lys	gca Ala 195	gct Ala	aaa Lys	gag Glu	atg Met	ctt Leu 200	gct Ala	aat Asn	tca Ser	gtt Val	aaa Lys	gag Glu 205	ctt Leu	aca Thr	agc Ser	624
cct Pro	gtt Val 210	gtg Val	gca Ala	gaa Glu	agt Ser	cca Pro 215	aaa Lys	aaa Lys	cct Pro	tcc Ser	atg Met 220	gta Val	aat Asn	aat Asn	tca Ser	672
ggg Gly 225	aaa Lys	gat Asp	ggg Gly	aat Asn	aca Thr 230	tct Ser	gca Ala	aat Asn	tct Ser	gct Ala 235	gat Asp	gag Glu	tct Ser	gtt Val	aaa Lys 240	720
ggg Gly	cct Pro	aat Asn	ctt Leu	aca Thr 245	gaa Glu	ata Ile	agt Ser	aaa Lys	aaa Lys 250	att Ile	aca Thr	gaa Glu	tct Ser	aac Asn 255	gca Ala	768
gtt Val	gtt Val	ctc Leu	gcc Ala 260	gtg Val	aaa Lys	gaa Glu	gtt Val	gaa Glu 265	act Thr	ttg Leu	ctt Leu	aca Thr	tct Ser	ata Ile	gat Asp	816
gag Glu	ctt Leu	gct Ala 275	aaa Lys	gct Ala	att Ile	ggt Gly	aaa Lys 280	aaa Lys	ata Ile	aaa Lys	aac Asn 285	gat Asp	gtt Val	agt Ser	tta Leu	864
gat Asp	aat Asn 290	gag Glu	gca Ala	gat Asp	cac His	aac Asn 295	gga Gly	tca Ser	tta Leu	ata Ile	tca Ser 300	gga Gly	gca Ala	tat Tyr	tta Leu	912
att Ile 305	tca Ser	aac Asn	tta Leu	ata Ile	aca Thr 310	aaa Lys	aaa Lys	ata Ile	agt Ser	gca Ala 315	ata Ile	aaa Lys	gat Asp	tca Ser	gga Gly 320	960
gaa	ttg	aag	gca	gaa	att	gaa	aag	gct	aag	aaa	tgt	tct	gaa	gaa	ttt	1008

Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe
 325 330 335

act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt 1056
 Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val
 340 345 350

act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa 1104
 Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys
 355 360 365

act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac 1152
 Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn
 370 375 380

ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt 1200
 Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu
 385 390 395 400

aca agc taa 1209
 Thr Ser *

<210> 80
 <211> 401
 <212> PRT
 <213> ospC Chimera

<400> 80
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 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
 20 25 30
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
 50 55 60
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala
 65 70 75 80
 Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr
 85 90 95
 Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser
 100 105 110
 Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys
 115 120 125
 Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys
 130 135 140
 Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala
 145 150 155 160
 Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly
 165 170 175
 Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys
 180 185 190
 Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
 195 200 205
 Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser Gly
 210 215 220

Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly
 225 230 235 240
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
 245 250 255
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu
 260 265 270
 Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp
 275 280 285
 Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile
 290 295 300
 Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu
 305 310 315 320
 Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr
 325 330 335
 Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr
 340 345 350
 Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr
 355 360 365
 Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu
 370 375 380
 Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr
 385 390 395 400
 Ser

<210> 81
 <211> 1205
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1205)

<400> 81
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205

cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca 672
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser
 210 215 220

gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa 720
 Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
 225 230 235 240

ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca 768
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
 245 250 255

gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat 816
 Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp
 260 265 270

gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt 864
 Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly
 275 280 285

tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat 912
 Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr
 290 295 300

aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca 960
 Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser
 305 310 315 320

006T99-34796560

gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat 1008
 Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp
 325 330 335

 ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat 1056
 Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn
 340 345 350

 gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct 1104
 Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala
 355 360 365

 aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa 1152
 Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu
 370 375 380

 aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag 1200
 Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu
 385 390 395 400

 ctt ac 1205
 Leu

<210> 82
 <211> 400
 <212> PRT
 <213> ospC Chimera

<400> 82
 Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
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 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
 20 25 30
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
 50 55 60
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala
 65 70 75 80
 Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr
 85 90 95
 Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser
 100 105 110
 Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys
 115 120 125
 Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys
 130 135 140
 Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala
 145 150 155 160
 Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly
 165 170 175
 Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys
 180 185 190
 Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
 195 200 205
 Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser Gly
 210 215 220

Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly
 225 230 235 240
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
 245 250 255
 Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu
 260 265 270
 Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu
 275 280 285
 Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr
 290 295 300
 Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu
 305 310 315 320
 Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe
 325 330 335
 Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val
 340 345 350
 Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys
 355 360 365
 Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn
 370 375 380
 Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
 385 390 395 400

<210> 83
 <211> 1236
 <212> DNA
 <213> ospC Chimera

<220>
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 1 5 10 15
 gca caa aaa ggt gct gag tca att gga tcc tgt agt aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys
 20 25 30
 ggt ggg gat tct gca tct act aat cct gct gac gag tct gcg aaa ggg 144
 Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly
 35 40 45
 cct aat ctt aca gaa ata agc aaa aaa att aca gat tct aat gca ttt 192
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
 50 55 60
 gta ctt gct gtt aaa gaa gtt gag act ttg gtt tta tct ata gat gaa 240
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu
 65 70 75 80
 ctt gct aag aaa gct att ggt caa aaa ata gac aat aat aat ggt tta 288
 Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu
 85 90 95

gct gct tta aat aat cag aat gga tct ttg tta gca gga gcc tat gca Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala															336
100110															
ata tca acc cta ata aca gaa aaa ttg agt aaa ttg aaa aat tta gaa Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu															384
115120125															
gaa tta aag aca gaa att gca aag gct aag aaa tgt tcc gaa gaa ttt Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe															432
130135140															
act aat aaa cta aaa agt ggt cat gca gat ctt ggc aaa cag gat gct Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala															480
145150155160															
acc gat gat cat gca aaa gca gct att tta aaa aca cat gca act acc Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr															528
165170175															
gat aaa ggt gct aaa gaa ttt aaa gat tta ttt gaa tca gta gaa ggt Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly															576
180185190															
ttg tta aaa gca gct caa gta gca cta act aat tca gtt aaa gaa ctt Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu															624
195200205															
aca agt cct gtt gta gca gaa agt cca aaa aaa cct cat atg gct aat Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn															672
210215220															
aat tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys															720
225230235240															
gga cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala															768
245250255															
ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ile Asp															816
260265270															
gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu															864
275280285															
gat aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu															912
290295300															
ata tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu															960
305310315320															
tta aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr															1008
325330335															

act aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag 1056
 Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln
 340 345 350

gat gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac 1104
 Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp
 355 360 365

aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg 1152
 Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu
 370 375 380

tca aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca 1200
 Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr
 385 390 395 400

aat cct gtt gtg gca gaa agt cca aaa aaa cct taa 1236
 Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro *
 405 410

<210> 84
 <211> 410
 <212> PRT
 <213> ospC Chimera

<400> 84
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 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys Gly
 20 25 30
 Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Val
 50 55 60
 Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu Leu
 65 70 75 80
 Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu Ala
 85 90 95
 Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110
 Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu Glu
 115 120 125
 Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr
 130 135 140
 Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala Thr
 145 150 155 160
 Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr Asp
 165 170 175
 Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly Leu
 180 185 190
 Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu Thr
 195 200 205
 Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn Asn
 210 215 220
 Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly
 225 230 235 240

[illegible]

RWW/SAB/ras
06/19/00

U.S. PTO
09/596746
06/19/00

Date: <u>6/19/00</u> EXPRESS MAIL LABEL NO. <u>EL387775380US</u>
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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s): Raymond J. Dattwyler, Gerald Seinost, Daniel Dykhuizen,
Benjamin J. Luft and Maria J. C. Gomes-Solecki

Title: GROUPS OF BORRELIA BURGDORFERI AND BORRELIA
AFZELII THAT CAUSE LYME DISEASE IN HUMANS

TRANSMITTAL OF SEQUENCE LISTING IN COMPUTER READABLE FORM
IN COMPLIANCE WITH 37 C.F.R. §§1.821(e) AND (f)

Box Patent Application
Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Transmitted herewith is a copy of the "Sequence Listing" in computer readable form as required by 37 C.F.R. §1.821(e). As required by 37 C.F.R. §1.821(f), Applicant's Attorney hereby states that the content of the "Sequence Listing" in paper form and of the computer readable form of the "Sequence Listing" are the same.

Respectfully submitted,

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Date: June 19, 2000

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